

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2006, 19:13:00 ; Search time 1515 Seconds
(without alignments)
11367.296 Million cell updates/sec

Title: US-10-656-598-1

Perfect score: 2470

Sequence: 1 ttggcgggcggaagcgccca.....ataaacaccatttgtgaatat 2470

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10409840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 8:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*
14: Geneseqn2005s:*
15: Geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2470	100.0	2470	6	ABL65811 Lung canc
2	2470	100.0	2470	6	Aai72250 KIAA0175
3	2470	100.0	2470	6	Abn95227 Gene #172
4	2470	100.0	2470	8	Abx76456 Lung canc
5	2470	100.0	2470	10	Abd80562 Ovarian c
6	2470	100.0	2470	10	Adc38346 Human pro
7	2470	100.0	2470	11	Adm39187 Cancer/an
8	2470	100.0	2470	11	Adm72650 Human TAS
9	2470	100.0	2470	12	Adm72216 Human TAS
10	2470	100.0	2470	12	Adn06035 Antipsori
11	2470	100.0	2470	12	Adl19824 Human sof
12	2470	100.0	2470	13	Adr25674 Breast ca
13	2470	100.0	2470	13	Adu05979 Novel bro
14	2470	100.0	2470	14	Adx07296 Cyclin-de
15	2470	100.0	2470	14	Adw93565 Human mat
16	2470	100.0	2470	14	Ady20529 DNA encod
17	2470	100.0	2470	14	Ady15427 DNA encod
18	2470	100.0	2470	14	Ady61853 Human gen

19	2470	100.0	2470	14	ABE57136
20	2470	100.0	2470	14	AEC82649
21	2470	100.0	2487	13	Adx51545 Plant ful
22	2470	100.0	2960	12	Adq23801 Human sof
23	2452	99.3	2463	13	Adx52219 Plant ful
24	2441	98.8	2441	13	Adx52095 Plant ful
25	2438	98.7	2453	8	ABx77595 Different
26	2438	98.7	2501	12	ADP07319 Human KIA
27	2438	98.7	2501	14	ADW93569 Human mat
28	2438	98.7	2501	15	AEE60929 Human pat
29	2438	98.7	2501	15	AEE83810 Human cDN
30	2438	98.7	2501	15	AEE71794 Human gen
31	2438	98.7	2510	14	ADW93566 Human mat
32	2253	91.2	2368	15	AEF71796 Human dia
33	2191.4	88.7	2391	13	ACN41843 Human dia
34	2190.6	88.7	2428	2	ABA92381 Human dom
35	2159.8	87.4	2519	8	ACA03961 cDNA down
36	2140.4	86.7	2583	13	ACN41839 Human dia
37	2137.4	86.5	2364	13	ACN41845 Human dia
38	2127.6	86.1	2162	6	ABK35345 Human cDN
39	2119.4	85.8	2372	13	ACN41844 Human dia
40	2107.4	85.3	2606	13	ACN41847 Human dia
41	2041	82.6	2251	15	AEF71798 Human gen
42	1956.4	79.2	2496	13	ACN41841 Human dia
43	1955.4	79.2	2530	13	ACN41840 Human dia
44	1952	79.0	2158	14	ADW93567 Human MEL
45	1896	76.8	2023	13	ADU66638 Human kin

ALIGNMENTS

RESULT 1

ABL65811
ID ABL65811 standard; DNA; 2470 BP.

XX ABL65811;

XX 15-MAY-2002 (first entry)

XX Lung cancer related gene sequence SEQ ID NO:4148.

XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.

XX Homo sapiens.

XX WO200194629-A2.

XX 13-DEC-2001.

XX 30-MAY-2001; 2001WO-US010838.

XX 05-JUN-2000; 2000US-0209473P.

XX 05-JUN-2000; 2000US-0209531P.

XX 18-SEP-2000; 2000US-0233133P.

XX 18-SEP-2000; 2000US-0233617P.

XX 20-SEP-2000; 2000US-0234009P.

XX 20-SEP-2000; 2000US-0234034P.

XX 22-SEP-2000; 2000US-0234052P.

XX 22-SEP-2000; 2000US-0234509P.

XX 25-SEP-2000; 2000US-0234567P.

XX 25-SEP-2000; 2000US-0234923P.

XX 25-SEP-2000; 2000US-0235077P.

XX 25-SEP-2000; 2000US-0235082P.

XX 25-SEP-2000; 2000US-0235134P.

XX 26-SEP-2000; 2000US-0235280P.

XX 26-SEP-2000; 2000US-0235637P.

XX 27-SEP-2000; 2000US-0235638P.

XX 27-SEP-2000; 2000US-0235711P.

Best Local Similarity 100.0%; Pred. No. 0;				Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	TTGGCGGGCGGAGCGGCCACACCGCGGATCGAAAGATTCTTAGGAACGCGGTACCA	60				
DB	1	TTGGCGGGCGGAGCGGCCACACCGCGGATCGAAAGATTCTTAGGAACGCGGTACCA	60				
QY	61	GC CGCGTCTCTCAGGACAGCAGGCGCCCTGTCTTCTGTGGGCGCGCTCAGCGGTGCC	120				
DB	61	GC CGCGTCTCTCAGGACAGCAGGCGCCCTGTCTTCTGTGGGCGCGCTCAGCGGTGCC	120				
QY	121	TCGCGCCCTCAGGTTCTTTTCTAAATCCAAATAAACTTGCAAGAGACTATGAAAGATT	180				
DB	121	TCGCGCCCTCAGGTTCTTTTCTAAATCCAAATAAACTTGCAAGAGACTATGAAAGATT	180				
QY	181	ATGATGAATCTTCAATATTATGAATACATGAAACTATTGGGACAGGTGGCTTGCAA	240				
DB	181	ATGATGAATCTTCAATATTATGAATACATGAAACTATTGGGACAGGTGGCTTGCAA	240				
QY	241	AGGTCAAACTTGGCTGCCATATCTTACTTGGAGAGATGGTAGCTATAAAATCATGGATA	300				
DB	241	AGGTCAAACTTGGCTGCCATATCTTACTTGGAGAGATGGTAGCTATAAAATCATGGATA	300				
QY	301	AAACACACTAGGAGTGATTTGCCCGGATCAAAACGGAGATGGAGGCTTGAAGAAC	360				
DB	301	AAACACACTAGGAGTGATTTGCCCGGATCAAAACGGAGATGGAGGCTTGAAGAAC	360				
QY	361	TGAGACATCAGCATATATGTCAACTCTACCATGTGCTAGAGCAGCCAAATATTCA	420				
DB	361	TGAGACATCAGCATATATGTCAACTCTACCATGTGCTAGAGCAGCCAAATATTCA	420				
QY	421	TGTTCTTGTAGTACTGCCCTGGAGGAGAGCTGTGTGACTATATAATTTCCAGGATCGCC	480				
DB	421	TGTTCTTGTAGTACTGCCCTGGAGGAGAGCTGTGTGACTATATAATTTCCAGGATCGCC	480				
QY	481	TGTCAGAGAGGAGACCGCGGTTGTCTTCGTCAGATAGTATCTGCTGTGCTTATGTGC	540				
DB	481	TGTCAGAGAGGAGACCGCGGTTGTCTTCGTCAGATAGTATCTGCTGTGCTTATGTGC	540				
QY	541	ACAGCCAGGCTATGTCTCAGGGACTCAAGCCAGCAAAATTTGCTTTGTATGATATC	600				
DB	541	ACAGCCAGGCTATGTCTCAGGGACTCAAGCCAGCAAAATTTGCTTTGTATGATATC	600				
QY	601	ATAAATTAAGCTGATTGACTTTGGTCTCTGTGCAAAACCCAAAGGCTTAAACAGGATTAC	660				
DB	601	ATAAATTAAGCTGATTGACTTTGGTCTCTGTGCAAAACCCAAAGGCTTAAACAGGATTAC	660				
QY	661	ATCTACAGACATGCTGTGGAGTCTGGCTTTATGACGACCTGAGTTAAATACAGGCAAT	720				
DB	661	ATCTACAGACATGCTGTGGAGTCTGGCTTTATGACGACCTGAGTTAAATACAGGCAAT	720				
QY	721	CATATCTTGATCAGAGGAGATGTTTGGAGCTGGCATCTGTTATATGTTCTTATGT	780				
DB	721	CATATCTTGATCAGAGGAGATGTTTGGAGCTGGCATCTGTTATATGTTCTTATGT	780				
QY	781	GTGGATTTCTACCATTTGATGATGATAATGTAATGGCTTTATACAAAGAGATTATCAGAG	840				
DB	781	GTGGATTTCTACCATTTGATGATGATAATGTAATGGCTTTATACAAAGAGATTATCAGAG	840				
QY	841	GAAAAATATGATGTGCCAAGTGTCTCTCCAGTAGCATCTGCTTCTTCAACAAATGC	900				
DB	841	GAAAAATATGATGTGCCAAGTGTCTCTCCAGTAGCATCTGCTTCTTCAACAAATGC	900				
QY	901	TGCAGGTGGACCAAGAAAGGATTTCTATGAAATCTTATTGAACCATCCCTGGATCA	960				
DB	901	TGCAGGTGGACCAAGAAAGGATTTCTATGAAATCTTATTGAACCATCCCTGGATCA	960				
QY	961	TGCAAGATTACAACTATCTCTGTGAGTGGCAAGCAAGATCTTTTATTCACCTCGATG	1020				
DB	961	TGCAAGATTACAACTATCTCTGTGAGTGGCAAGCAAGATCTTTTATTCACCTCGATG	1020				
QY	1021	ATGATTCGGTAAACAGAACTTTCTGTATCATCAGAAACAAACGAGCAAAATAGGAGATT	1080				

1021	ATGATTCGGTAAACAGAACTTTCTGTATCATCAGAAAAACAGGCAAAACAAATGGAGGTT	1080
1081	TAAATTTCACTGTGGCAGTATGATCACTCAGCGCTACCTATCTTCTGTCTTAGCCA	1140
1081	TAAATTTCACTGTGGCAGTATGATCACTCAGCGCTACCTATCTTCTGTCTTAGCCA	1140
1141	AGGCTCGGGGAAAAACAAGTTCTTAAAGCTTTCTTCTTCTCTCTGTGACAAGCCAC	1200
1141	AGGCTCGGGGAAAAACAAGTTCTTAAAGCTTTCTTCTTCTCTCTGTGACAAGCCAC	1200
1201	CTACCCCATTCACAGACATCAAGTCAAAATTTGGAGTCTGGAAGATGACGCGCAAC	1260
1201	CTACCCCATTCACAGACATCAAGTCAAAATTTGGAGTCTGGAAGATGACGCGCAAC	1260
1261	ATAAAATTTATCTGCGGGATTAAATAGACTATGATTTGGTGTGCAAGATGATTATCAA	1320
1261	ATAAAATTTATCTGCGGGATTAAATAGACTATGATTTGGTGTGCAAGATGATTATCAA	1320
1321	GTGCTGCTACTCCCCGAAACATCAAGTTTACAAAGTACTGGAAGATGATGATGATGAT	1380
1321	GTGCTGCTACTCCCCGAAACATCAAGTTTACAAAGTACTGGAAGATGATGATGATGAT	1380
1381	AATCTAATCATTTAATCCAGCTTATGCAAGAACACCTGCAAAATAAATTAAGAACPAAG	1440
1381	AATCTAATCATTTAATCCAGCTTATGCAAGAACACCTGCAAAATAAATTAAGAACPAAG	1440
1441	AAAAATGATATCTCTTAAGTCTGTAAAGAAATGAAGAGTACTTTATGTTTCTGAGC	1500
1441	AAAAATGATATCTCTTAAGTCTGTGTAAAGAAATGAAGAGTACTTTATGTTTCTGAGC	1500
1501	CAAGAGTCCAGTTAATGAACACAGCATTAAGAGAGAAATCTCACTACGCCAATCGTT	1560
1501	CAAGAGTCCAGTTAATGAACACAGCATTAAGAGAGAAATCTCACTACGCCAATCGTT	1560
1561	ACACTACACCTTCAAAAGCTGAAACCCAGTCTGAAAGAACTCCAAATTAATTAAT	1620
1561	ACACTACACCTTCAAAAGCTGAAACCCAGTCTGAAAGAACTCCAAATTAATTAAT	1620
1621	TAAATTCACAGGAAACAGACAAAGTTAATGACAGGTGTCTATTAGCCCTGAGAGCGGTGCC	1680
1621	TAAATTCACAGGAAACAGACAAAGTTAATGACAGGTGTCTATTAGCCCTGAGAGCGGTGCC	1680
1681	GCTCAGTGGAAATGGAATCCAAAGCACAATATGAGAGAGACTCCAAAAAGAAAGGAG	1740
1681	GCTCAGTGGAAATGGAATCCAAAGCACAATATGAGAGAGACTCCAAAAAGAAAGGAG	1740
1741	CCAAAGTGTGGGAGCTTGAAGGGGTTGATAAGGTATCACTGCTCACCAGCA	1800
1741	CCAAAGTGTGGGAGCTTGAAGGGGTTGATAAGGTATCACTGCTCACCAGCA	1800
1801	GCAAAAGGAAGGTTCTGCCAGAGACGGGCCAGAGACTTAAAGCTTCACTATAATGTA	1860
1801	GCAAAAGGAAGGTTCTGCCAGAGACGGGCCAGAGACTTAAAGCTTCACTATAATGTA	1860
1861	CTACAACTAGATTAGTGAATCCAGATCAACTGTGTGTAATGAAATTAATGTTCTTCCAA	1920
1861	CTACAACTAGATTAGTGAATCCAGATCAACTGTGTGTAATGAAATTAATGTTCTTCCAA	1920
1921	AGAGCATGTTGACTTTGTACAAAAGGGTTATACACTGAAGTGTCAACACAGTCAAGATT	1980
1921	AGAGCATGTTGACTTTGTACAAAAGGGTTATACACTGAAGTGTCAACACAGTCAAGATT	1980
1981	TTGGGAAAGTGAACAATGCAATTTGAATTAAGAGTGTGCCAGCTTCAAAAACCCGATGTG	2040
1981	TTGGGAAAGTGAACAATGCAATTTGAATTAAGAGTGTGCCAGCTTCAAAAACCCGATGTG	2040
2041	TGGGTATCAGGAGGACGCGCTTAAAGGCGATGCTCGGTTTACAAAAAGATTAGTGGAG	2100
2041	TGGGTATCAGGAGGACGCGCTTAAAGGCGATGCTCGGTTTACAAAAAGATTAGTGGAG	2100
2101	ACATCCCTATCTAGTGCAGAGGTATATTCATGATTTCTTCCATCTCTCCGCGATGATGTG	2160
2101	ACATCCCTATCTAGTGCAGAGGTATATTCATGATTTCTTCCATCTCTCCGCGATGATGTG	2160

QY 2161 GGTGTGATACAGCTACATAAGACCTGTTATGATCGCTTTGATTTAAAGTTCATTGGAA 2220
 DB 2161 GGTGTGATACAGCTACATAAGACCTGTTATGATCGCTTTGATTTAAAGTTCATTGGAA 2220
 QY 2221 CTACCAACTTGTGTTCTTAAGAGCTATCTTAAGACCAATATCTCTTTGTTTAAACAAA 2280
 DB 2221 CTACCAACTTGTGTTCTTAAGAGCTATCTTAAGACCAATATCTCTTTGTTTAAACAAA 2280
 QY 2281 GATATTATTTGTTGTAAGTAATCAAGCCCATCTGTCATATATGTTACTGTCTTTT 2340
 DB 2281 GATATTATTTGTTGTAAGTAATCAAGCCCATCTGTCATATATGTTACTGTCTTTT 2340
 QY 2341 TAATCATGTGTTTGTATATTAATTAATGTTGACCTTCTTAGATTCACCTTCCATATGTG 2400
 DB 2341 TAATCATGTGTTTGTATATTAATTAATGTTGACCTTCTTAGATTCACCTTCCATATGTG 2400
 QY 2401 AATGTAAGCTCTTAAGTATGTCCTTTGTAAGTGTAAATTTCTTCTGAAATAAACCAT 2460
 DB 2401 AATGTAAGCTCTTAAGTATGTCCTTTGTAAGTGTAAATTTCTTCTGAAATAAACCAT 2460
 QY 2461 TTGTGAATAT 2470
 DB 2461 TTGTGAATAT 2470

RESULT 3

ABN95227
 ID ABN95227 standard; DNA; 2470 BP.
 AC ABN95227;

DT 13-AUG-2002 (first entry)

DE Gene #1725 used to diagnose liver cancer.

KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
 KW metastatic liver tumour; cycostatic; expression profile; disease state;
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.

OS Homo sapiens.

PN WO200229103-A2.

XX 11-APR-2002.

XX 02-OCT-2001; 2001WO-US030589.

XX 02-OCT-2000; 2000US-0237054P.

XX (GENE-) GENE LOGIC INC.

PA Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;

PI WPI; 2002-426119/45.

XX Diagnosing and detecting the progression of liver cancer, hepatocellular
 PT carcinoma or metastatic liver tumor in a patient, involves detecting the
 PT level of expression of two or more genes in a liver tissue sample.

PS Claim 1; SEQ ID NO 1725; 298pp; English.

XX The invention relates to a novel method for diagnosing and detecting the
 CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
 CC tumour in a patient, and differentiating metastatic liver cancer from
 CC hepatocellular carcinoma in a patient, involving detecting the level of
 CC expression of two or more genes represented in ABN9503-ABN97455 in a
 CC tissue sample. The method of the invention has hepatotropic, and
 CC cytostatic activity. The method is useful for diagnosing and detecting
 CC the progression of liver cancer, hepatocellular carcinoma and metastatic
 CC liver carcinoma in a patient. The method is useful for identifying
 CC expression profiles which serve as useful diagnostic markers as well as
 CC markers that can be used to monitor disease states, disease progression,

CC drug toxicity, drug efficacy and drug metabolism. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 2470 BP; 767 A; 488 C; 536 G; 679 T; 0 U; 0 Other;

Query Match 100.0%; Score 2470; DB 6; Length 2470;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGGGGGGAAGCGGCCACACCGCGGATCGAAGAGTTCTTAGGAACCGCGTACCA 60

DB 1 TTGGGGGGGGAAGCGGCCACACCGCGGATCGAAGAGTTCTTAGGAACCGCGTACCA 60

QY 61 GCCGGGTCTCTCAGGACAGCGGCCCTGCTCTTGTGGGGCGCGCTCAGCGGTGCC 120

DB 61 GCCGGGTCTCTCAGGACAGCGGCCCTGCTCTTGTGGGGCGCGCTCAGCGGTGCC 120

QY 121 TCCGCCCTCAGGTCTTTTCTAATTCAAATAAACTTGCAGAGGACTATGAAGAAT 180

DB 121 TCCGCCCTCAGGTCTTTTCTAATTCAAATAAACTTGCAGAGGACTATGAAGAAT 180

QY 181 ATGATGAACCTTCTCAATATTAATGAATACATGAATTTGGGACAGGTGGCTTGC 240

DB 181 ATGATGAACCTTCTCAATATTAATGAATACATGAATTTGGGACAGGTGGCTTGC 240

QY 241 AGGTCAAACTTGCCTGCCATATCTTACTGGAGAGATGGTAGCTATAAATAATCATG 300

DB 241 AGGTCAAACTTGCCTGCCATATCTTACTGGAGAGATGGTAGCTATAAATAATCATG 300

QY 301 AAAACACACTAGGGAGTGATTTGCCCGGATCAAAACCGGAGATTGAGGCTTTGAAGA 360

DB 301 AAAACACACTAGGGAGTGATTTGCCCGGATCAAAACCGGAGATTGAGGCTTTGAAGA 360

QY 361 TGAGACATCAGCATATATGTCAACTTCACTACCTAGTAGAGACAGCAACCAATTTCA 420

DB 361 TGAGACATCAGCATATATGTCAACTTCACTACCTAGTAGAGACAGCAACCAATTTCA 420

QY 421 TGGTCTTGGTACTGCTCCCTGGAGGAGAGCTGTTTGACTATATAATTTCCAGGATCG 480

DB 421 TGGTCTTGGTACTGCTCCCTGGAGGAGAGCTGTTTGACTATATAATTTCCAGGATCG 480

QY 481 TGTCAAGAGAGAGACCCGGGTTGTTCCGTCAGATAGTATCTGCTGTGTTGATGTC 540

DB 481 TGTCAAGAGAGAGACCCGGGTTGTTCCGTCAGATAGTATCTGCTGTGTTGATGTC 540

QY 541 ACAGCCAGGGCTATGCTCAGGAGACCTCAAGCCAGAAAAATTTGCTGTTGATGATATC 600

DB 541 ACAGCCAGGGCTATGCTCAGGAGACCTCAAGCCAGAAAAATTTGCTGTTGATGATATC 600

QY 601 ATAAATTAAGCTGATTGACATTTGCTCTGTGCAAAACCCCAAGGTAACAGGATTA 660

DB 601 ATAAATTAAGCTGATTGACATTTGCTCTGTGCAAAACCCCAAGGTAACAGGATTA 660

QY 661 ATCTACAGACATGCTGTGGAGTCTGGCTTATGACAGCACCTGAGTTAATACAAGCA 720

DB 661 ATCTACAGACATGCTGTGGAGTCTGGCTTATGACAGCACCTGAGTTAATACAAGCA 720

QY 721 CATATCTTGGATCAGAGCAGATGTTTGAGCATGGGCATCTGTTATATGTTCTTATGT 780

DB 721 CATATCTTGGATCAGAGCAGATGTTTGAGCATGGGCATCTGTTATATGTTCTTATGT 780

QY 781 GTGATTTTCTACCATTTGATGATGATGTAATGGCTTTTATACAAGAGATTAAGAG 840

DB 781 GTGATTTTCTACCATTTGATGATGATGTAATGGCTTTTATACAAGAGATTAAGAG 840

QY 841 GAAATATGATGTTTCCCAAGTGGCTCTCTCCAGTAGCATCTGCTTCTTCAACAAATGC 900

DB 841 GAAATATGATGTTTCCCAAGTGGCTCTCTCCAGTAGCATCTGCTTCTTCAACAAATGC 900

QY 901 TGCAGGTGACCAAGAAAAAGGATTTCTATGAAAAATCTATTGAAACCATCTCGGTATCA 960

DB 901 TGCAGGTGACCAAGAAAAAGGATTTCTATGAAAAATCTATTGAAACCATCTCGGTATCA 960

901	TGCAAGGTGGACCCAAAGAAACGGATTTCTATGAATAAATCTATTGAACCATTCCTCGTGCATCA	960
961	TGCAAGATTACAATCTATCCTGTTGAGTGGCAAAGCAAGAATCCCTTTATTTCACCTCGATG	1020
961	TGCAAGATTACAATCTATCCTGTTGAGTGGCAAAGCAAGAATCCCTTTATTTCACCTCGATG	1020
1021	ATGATTTGGTTAACAGAACTTTCTGTATCATCACAGAAAACAAGGCCAAACAATGGAGATT	1080
1021	ATGATTTGGTTAACAGAACTTTCTGTATCATCACAGAAAACAAGGCCAAACAATGGAGATT	1080
1081	TAAATTTCACTGTGGCAGTATGATCACCCTCAGCGTACTATCTTCTGCTTCTTAGCCAAGA	1140
1081	TAAATTTCACTGTGGCAGTATGATCACCCTCAGCGTACTATCTTCTGCTTCTTAGCCAAGA	1140
1141	AGGCTCGGGGAAAAACCAAGTTCTGTTTTAAGGCTTTCTTTCTCTCTGTGGACAAGCCAGTG	1200
1141	AGGCTCGGGGAAAAACCAAGTTCTGTTTTAAGGCTTTCTTTCTCTCTGTGGACAAGCCAGTG	1200
1201	CTACCCCATTACAGACATCAAGTCAAATAATTGGAGTCTGGAGAGTGTGACCGCAAGTG	1260
1201	CTACCCCATTACAGACATCAAGTCAAATAATTGGAGTCTGGAGAGTGTGACCGCAAGTG	1260
1261	ATAAAATTATGTGGCGGATTATAGACTATGATTTGGTGTGAAGATGATTTATCAACAG	1320
1261	ATAAAATTATGTGGCGGATTATAGACTATGATTTGGTGTGAAGATGATTTATCAACAG	1320
1321	GTGCTGTCTACTCCCGAACATCAAGTTTACCAAGTACTGCGACAGAAATCAATGGGGTGG	1380
1321	GTGCTGTCTACTCCCGAACATCAAGTTTACCAAGTACTGCGACAGAAATCAATGGGGTGG	1380
1381	AATCTAAATCATTAATCTCCAGCCTTATGCAGAAACACCTGCAAAATAAATTAAGAAACAAAG	1440
1381	AATCTAAATCATTAATCTCCAGCCTTATGCAGAAACACCTGCAAAATAAATTAAGAAACAAAG	1440
1441	AAAATGTATATATCTCTTAAGTCTGCTGTAAAGAAATGAAGATGACTTTATGTTCTTCTGAGC	1500
1441	AAAATGTATATATCTCTTAAGTCTGCTGTAAAGAAATGAAGATGACTTTATGTTCTTCTGAGC	1500
1501	CAAAGACTCCAGTTTAAATPAGBAACAGAGATTAAGAGAGAAATCACTCACTACGCCAAATCGTT	1560
1501	CAAAGACTCCAGTTTAAATPAGBAACAGAGATTAAGAGAGAAATCACTCACTACGCCAAATCGTT	1560
1561	ACACTACACCCCTCAAAAGCTAGAAAACCAAGTGCCTGAAAGAAATCCCAATTTAAATATACCAG	1620
1561	ACACTACACCCCTCAAAAGCTAGAAAACCAAGTGCCTGAAAGAAATCCCAATTTAAATATACCAG	1620
1621	TAAATTTCAACAGGAACAGACAAGTTAATGACAGTGTCTATTAGCCCTGAGAGCGGTGCC	1680
1621	TAAATTTCAACAGGAACAGACAAGTTAATGACAGTGTCTATTAGCCCTGAGAGCGGTGCC	1680
1681	GCTCAGTGGAAATGGATCTCAACAGCACATATGGAGGAGACTCCAAAAGAAAGAGGAG	1740
1681	GCTCAGTGGAAATGGATCTCAACAGCACATATGGAGGAGACTCCAAAAGAAAGAGGAG	1740
1741	CAAAAGTGTTTGGGAGCCTTGAAAAGGGGTTTGGATAAGGTTATCACTGTGCTCACACAGGA	1800
1741	CAAAAGTGTTTGGGAGCCTTGAAAAGGGGTTTGGATAAGGTTATCACTGTGCTCACACAGGA	1800
1801	GAAAAGGAAGGGTTCTGCCAGAGACAGCGGCCAGAGAATAAGGTTTCACTAATATGTGA	1860
1801	GAAAAGGAAGGGTTCTGCCAGAGACAGCGGCCAGAGAATAAGGTTTCACTAATATGTGA	1860
1861	CTACNACTAGATTAGTGAATCCAGATCAACTGTTTGAATGAATAATGCTCTATTCTTCCAA	1920
1861	CTACNACTAGATTAGTGAATCCAGATCAACTGTTTGAATGAATAATGCTCTATTCTTCCAA	1920
1921	AGAAGCATGTTGACTTTTGTAACAAAGGGTTATACACTGMAAGTGTCAAAACAGATCAGATT	1980
1921	AGAAGCATGTTGACTTTTGTAACAAAGGGTTATACACTGMAAGTGTCAAAACAGATCAGATT	1980
1981	TTGGGAAAGTGACAAATGCAATTTTGAATTTAGAAGTGTGCCAGCTTTCAAAAACCGGATGTGG	2040
1981	TTGGGAAAGTGACAAATGCAATTTTGAATTTAGAAGTGTGCCAGCTTTCAAAAACCGGATGTGG	2040

RESULT 4
ABX76456

ABX/8436
ID ABX76456 standard: DNA: 2470 BP.

AC ABX76456;

DT 02-APR-2003 (first entry)

XX DE Lung cancer-associated polynucleotide #320.

XX Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX Unidentified.

XX PN WO200286443-A2.

XX 31-OCT-2002.
PD

18-APR-2002: 2002WO-US012476.

XX
PR 18-APR-2001: 2001US-0284770P.

PR 18-APR-2001; 2001US-0284770F;
PR 10-MAY-2001; 2001US-0290492P;

PR 09-NOV-2001; 2001US-0339245P.

PR 13-NOV-2001; 2001US-0350666P.

PR 29-NOV-2001; 2001US-0334370P.

PR 12-APR-2002; 2002US-0372246P.

PA (EOSB-) EOS BIOTECHNOLOGY INC.

PI Aziz N, Murray R;

DR WPI; 2003-093161/08.

DR P-PSDB; ABU56727.

PT Detecting a lung cancer-associated transcript in a cell from a patient

PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PS expression in lung cancer.
XX
XX
XX
XX

Claim 22; Page 436; 453pp; English.

CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridizes
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
CC invention
XX

SQ Sequence 2470 BP; 767 A; 488 C; 536 G; 679 T; 0 U; 0 Other;

Query Match 100.0%; Score 2470; DB 8; Length 2470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TTGGCGGGGGAAGCGGCCCAACCCGGCGATCGAAAGATTCTTAGGAACGCGTACCA	60
DB	1	TTGGCGGGGGAAGCGGCCCAACCCGGCGATCGAAAGATTCTTAGGAACGCGTACCA	60
QY	61	GCCGCGTCTCTCAGGACAGACAGCGCCCTGTCTTCTGTGGGGCGCGCTCAGCGGTGCC	120
DB	61	GCCGCGTCTCTCAGGACAGACAGCGCCCTGTCTTCTGTGGGGCGCGCTCAGCGGTGCC	120
QY	121	TCCGCGCCCTCAGGTCTCTTTTCTTAATTCAAAATAAACTTGCAGAGAGACTATGAAAGATT	180
DB	121	TCCGCGCCCTCAGGTCTCTTTTCTTAATTCAAAATAAACTTGCAGAGAGACTATGAAAGATT	180
QY	181	ATGATGAACCTTCTCAAATATTAATGAAATACATGAACATAATGGACAGGTGGCTTTCGAA	240
DB	181	ATGATGAACCTTCTCAAATATTAATGAAATACATGAACATAATGGACAGGTGGCTTTCGAA	240
QY	241	AGGTCAAACTTGCTGCGCATATCTTCTACTGGAGAGATGGTAGCTATAAAATCATGGATA	300
DB	241	AGGTCAAACTTGCTGCGCATATCTTCTACTGGAGAGATGGTAGCTATAAAATCATGGATA	300
QY	301	AAAAACACTTAGGGAGTGATTTCGCCCGGATCAAAACGGAGATTGAGGCTTGAAGAACC	360
DB	301	AAAAACACTTAGGGAGTGATTTCGCCCGGATCAAAACGGAGATTGAGGCTTGAAGAACC	360
QY	361	TGAGACATCAGCATATATGTCAACTCTACCATGTGTAGAGACAGCCACAAAATTTC	420
DB	361	TGAGACATCAGCATATATGTCAACTCTACCATGTGTAGAGACAGCCACAAAATTTC	420
QY	421	TGTTCTTGAGTACTGCTGCGTGGAGGAGCTGTTTGACTATATATAATTTCCAGGATCGCC	480
DB	421	TGTTCTTGAGTACTGCTGCGTGGAGGAGCTGTTTGACTATATATAATTTCCAGGATCGCC	480
QY	481	TGTCAGAGAGGAGACCGGGTGTCTTCGTCAGATAGTATCTGCTGTGCTTATGTGC	540
DB	481	TGTCAGAGAGGAGACCGGGTGTCTTCGTCAGATAGTATCTGCTGTGCTTATGTGC	540
QY	541	ACAGCCAGGGCTATGTCTCAGGAGGACTCAAGCCAGAAAAATTTGCTGTTTGTGATATC	600
DB	541	ACAGCCAGGGCTATGTCTCAGGAGGACTCAAGCCAGAAAAATTTGCTGTTTGTGATATC	600
QY	601	ATAAATTAAGCTGATTGACTTTTGGTCTCTGTGCAAAACCCAAAGGCTAAAGGATTACC	660

Db 361 TGAGCATCAGCATATATGTCACACTCTACATGCTGCTAGAGACGCAACAAATATTC 420
Qy 421 TGGTTCTTGAGTACTGCCCTGGAGGAGAGCTGTTTGACTATATAATATTTCCAGGATCGCC 480
Db 421 TGGTTCTTGAGTACTGCCCTGGAGGAGAGCTGTTTGACTATATAATATTTCCAGGATCGCC 480
Qy 481 TGTCAAGAGGAGACCGGGTGTCTTCGTCAGATAGTATCTGCTGTTGCTTATGTGC 540
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Qy 541 ACAGCCAGGCTATGCTCAAGGAGCTCAAGCCAGCAAAATTTGCTGTTGATGAATATC 600
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Db 601 ATAAATTAAGCTGATGATGCTTGGTCTCTGTGCAAAACCCAGGGTAAACAAGGATTAAC 660
Qy 661 ATCTACAGATGCTGCTGGAGTCTGGCTTATGTCAGACCTGATGTTAAATACAGGCAAT 720
Db 661 ATCTACAGATGCTGCTGGAGTCTGGCTTATGTCAGACCTGATGTTAAATACAGGCAAT 720
Qy 721 CATATCTCGATCAGAGGAGATGTTTGGAGCATGGGCATCTGTTATATGTTCTTATGT 780
Db 721 CATATCTCGATCAGAGGAGATGTTTGGAGCATGGGCATCTGTTATATGTTCTTATGT 780
Qy 781 GTGGATTTCTACCATTTGATGATGATGTAATGTAATGTAATGTAATGTAATGTAATG 840
Db 781 GTGGATTTCTACCATTTGATGATGATGTAATGTAATGTAATGTAATGTAATGTAATG 840
Qy 841 GAAATATGATGTTCCCAAGTGGCTCTCCAGTAGCATCTGCTTCTTCAACAAATGC 900
Db 841 GAAATATGATGTTCCCAAGTGGCTCTCCAGTAGCATCTGCTTCTTCAACAAATGC 900
Qy 901 TGCAGGTGACCCAAAGAAACGGATTTCTATGAAATCTATTTGAACCATCCCTGGATCA 960
Db 901 TGCAGGTGACCCAAAGAAACGGATTTCTATGAAATCTATTTGAACCATCCCTGGATCA 960
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Db 961 TGCAGATTAACAATCTCTGTTGAGTGCAAGCAAGATCTTTTATTCACCTCGATG 1020
Qy 1021 ATGATTGCGTAACAGAACTTCTGTATCATCAAGAAACCAAGCAAGCAAGATGAGGAT 1080
Db 1021 ATGATTGCGTAACAGAACTTCTGTATCATCAAGAAACCAAGCAAGCAAGATGAGGAT 1080
Qy 1081 TAATTTCACTGTGGCAGTATGATCACCTCAGGCTACCTATCTTCTGCTTCTAGCCAAG 1140
Db 1081 TAATTTCACTGTGGCAGTATGATCACCTCAGGCTACCTATCTTCTGCTTCTAGCCAAG 1140
Qy 1141 AGGCTCGGGGAAAACAGTTCTGTTTAAAGCTTTCTTTCTTCTGTCGACCAAGCCAGTG 1200
Db 1141 AGGCTCGGGGAAAACAGTTCTGTTTAAAGCTTTCTTTCTTCTGTCGACCAAGCCAGTG 1200
Qy 1201 CTACCCCAATTCACAGATCAAGTCAAAATTAATGAGTCTGGAAGATGTGACCGCAAGTG 1260
Db 1201 CTACCCCAATTCACAGATCAAGTCAAAATTAATGAGTCTGGAAGATGTGACCGCAAGTG 1260
Qy 1261 ATAAATTAATGTCGGGGATTAATAGACTATGATGTTGGTGAAGTATGTTTATCAACAG 1320
Db 1261 ATAAATTAATGTCGGGGATTAATAGACTATGATGTTGGTGAAGTATGTTTATCAACAG 1320
Qy 1321 GTGCTGCTACTCCCGGAAACATCACAGTTTACCAAGTACTGGAAGCAAGTGGGGTGG 1380
Db 1321 GTGCTGCTACTCCCGGAAACATCACAGTTTACCAAGTACTGGAAGCAAGTGGGGTGG 1380
Qy 1381 AATCTAAATCATTAATCTCAGCTTATGAGAAACACCTGCAAAATAAATTAAGAAACAAG 1440
Db 1381 AATCTAAATCATTAATCTCAGCTTATGAGAAACACCTGCAAAATAAATTAAGAAACAAG 1440
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Db 1441 AAAATGTATATCTCTTAAGTCTGCTGTAAGAAATGAAGAGTACTTATGTTCTGAGC 1500
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Db 1621 TAAATTTCAACAGGAACAGACAAGTTAATGACAGGTGTCAATAGCCCTGAGAGCCGTGCC 1680
Qy 1681 GCTCAGTGGAAATGGATCTCAACCAAGCACATATGGAGGAGACTCCAAAAGAAAGGGAG 1740
Db 1681 GCTCAGTGGAAATGGATCTCAACCAAGCACATATGGAGGAGACTCCAAAAGAAAGGGAG 1740
Qy 1741 CCAAAGTGTGGAGCCCTTGAAGGGGTGGATAAGTTATCACTGTGCTCAACAGGA 1800
Db 1741 CCAAAGTGTGGAGCCCTTGAAGGGGTGGATAAGTTATCACTGTGCTCAACAGGA 1800
Qy 1801 GCAAAAGGAAGGTTCTGCCAGAGACGGGCCAGAGACTTAAAGCTTCACTATAATGTA 1860
Db 1801 GCAAAAGGAAGGTTCTGCCAGAGACGGGCCAGAGACTTAAAGCTTCACTATAATGTA 1860
Qy 1861 CTACAACTAGATAGTGAATCCAGATCAACTGTTGAAATGAATATGTTCTTCCAA 1920
Db 1861 CTACAACTAGATAGTGAATCCAGATCAACTGTTGAAATGAATATGTTCTTCCAA 1920
Qy 1921 AGAGCATGTTGACTTGTACAAAGGGTTATACACTGAAAGTGTCAACACAGTCAAGT 1980
Db 1921 AGAGCATGTTGACTTGTACAAAGGGTTATACACTGAAAGTGTCAACACAGTCAAGT 1980
Qy 1981 TTGGGAAAGTACAAATGCAATTTGAAATTAAGTGTGCCAGCTTCAAAAACCCGATGG 2040
Db 1981 TTGGGAAAGTACAAATGCAATTTGAAATTAAGTGTGCCAGCTTCAAAAACCCGATGG 2040
Qy 2041 TGGGTATCAGGAGGAGCGGCTTAAAGGGCGATGCTTGGGTTTACAAAAGATAGTGGAG 2100
Db 2041 TGGGTATCAGGAGGAGCGGCTTAAAGGGCGATGCTTGGGTTTACAAAAGATAGTGGAG 2100
Qy 2101 ACATCTATCTAGTGAAGGTATAATGATGAGTCTTCCATCTGCGGATGAGTGTG 2160
Db 2101 ACATCTATCTAGTGAAGGTATAATGATGAGTCTTCCATCTGCGGATGAGTGTG 2160
Qy 2161 GGTGTGATACAGCTTACATAAGACTGTTATGATGCTTTCATTTTAAAGTTCATTGGAA 2220
Db 2161 GGTGTGATACAGCTTACATAAGACTGTTATGATGCTTTCATTTTAAAGTTCATTGGAA 2220
Qy 2221 CTACCAACTTGTCTTAAAGAGCTATCTTAAAGCAATATCTCTTGTGTTTAAACAAA 2280
Db 2221 CTACCAACTTGTCTTAAAGAGCTATCTTAAAGCAATATCTCTTGTGTTTAAACAAA 2280
Qy 2281 GATATATTTTGTGATGAATCTAAATCAAGCCCATCTGTCATATGTTACTGTCTTTT 2340
Db 2281 GATATATTTTGTGATGAATCTAAATCAAGCCCATCTGTCATATGTTACTGTCTTTT 2340
Qy 2341 TAATCATGCTGTTTGTATATTAATTAATGTTGATCTTCTTAGATTTCACTTCCATATG 2400
Db 2341 TAATCATGCTGTTTGTATATTAATTAATGTTGATCTTCTTAGATTTCACTTCCATATG 2400
Qy 2401 AATGTAAGCTTAACTATGCTCTTGTGTAATGTTAAATTTCTTCTGAAATAAACCAT 2460
Db 2401 AATGTAAGCTTAACTATGCTCTTGTGTAATGTTAAATTTCTTCTGAAATAAACCAT 2460
Qy 2461 TTGTGAATAT 2470
Db 2461 TTGTGAATAT 2470

ID ADE38346 standard; DNA; 2470 BP.
AC ADE38346;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human protein 2089 gene sequence.
DE
DE tumorigenic disorder; angiogenic disorder; aberrant gene expression;
KW aberrant protein activity; cytostatic; antithyroid; antidiabetic;
KW ophthalmological; cancer; breast cancer; colon cancer; lung cancer;
KW prostatic cancer; Grave's disease; diabetic retinopathy; gene; ds;
KW protein 2089.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT 171..2126
FT CDS /tag= a
FT /product= "Human protein 2089"
FT
PN WO2003065006-A2.
XX
XX 07-AUG-2003.
XX
XX 30-JAN-2003; 2003WO-US002588.
PF
XX 31-JAN-2002; 2002US-0353600P.
PR 15-MAR-2002; 2002US-0364517P.
PR 09-APR-2002; 2002US-0371075P.
PR 10-APR-2002; 2002US-0371507P.
PR 16-APR-2002; 2002US-0372984P.
PR 19-APR-2002; 2002US-0374194P.
PR 24-MAY-2002; 2002US-0382955P.
PR 31-MAY-2002; 2002US-0385023P.
PR 14-JUN-2002; 2002US-0388533P.
PR 17-JUN-2002; 2002US-0389395P.
PR 25-JUN-2002; 2002US-0391324P.
PR 15-JUL-2002; 2002US-0395944P.
PR 22-JUL-2002; 2002US-0397726P.
PR 13-AUG-2002; 2002US-0403046P.
PR 22-AUG-2002; 2002US-0405155P.
PR 27-AUG-2002; 2002US-0406361P.
PR 25-OCT-2002; 2002US-0421195P.
PR 12-NOV-2002; 2002US-0425456P.
PR 19-NOV-2002; 2002US-0427626P.
PR 10-DEC-2002; 2002US-0432122P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Hunter JJ, Macbeth KJ, Tsai P, Lesoon A, Lightcap ES;
PI Williamson MW, Rudolph-Owen LA;
PI
XX
XX WPI; 2003-646176/61.
DR P-PSDB; ADE38347.
XX
XX Treating subject having tumorigenic disorder or angiogenic disorder
PT caused by aberrant polypeptide e.g., N-formylpeptide receptor or nucleic
PT acid, by administering a modulator.
XX
XX Disclosure; SEQ ID NO 7; 454pp; English.
XX
XX This invention relates to a novel method of treating a human subject
CC having a tumorigenic disorder or angiogenic disorder, caused by aberrant
CC gene expression or activity of an isolated protein, by administering a
CC modulator. The modulator may have cytostatic, antithyroid, antidiabetic
CC or ophthalmological activity. The method is useful for treating a subject
CC having a tumorigenic or angiogenic disorder, in particular for treating
CC cancer (for example breast cancer, colon cancer, lung cancer or prostatic
CC cancer) and, for example, Grave's disease and diabetic retinopathy. The
CC present sequence is a DNA sequence which encodes the novel isolated human
CC protein 2089 of the invention.
XX

SQ	Sequence	2470 BP; 767 A; 488 C; 536 G; 679 T; 0 U; 0 Other;
	Query Match	100.0%; Score 2470; DB 10; Length 2470;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 2470; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	TTGGCGGGGGAAGCGGCCACAAACCCGGCGATCGAAAGATTCTTTAGGAACCCCGTACCA 60
DB	1	TTGGCGGGGGAAGCGGCCACAAACCCGGCGATCGAAAGATTCTTTAGGAACCCCGTACCA 60
QY	61	GGCGGTCTCTCAGACAGCAGGCCCTCTGCTCTCTGCGGCGCGCTCAGCCGTGCC 120
DB	61	GGCGGTCTCTCAGACAGCAGGCCCTCTGCTCTCTGCGGCGCGCTCAGCCGTGCC 120
QY	121	TCGCGCCCTCAGGTCTCTTTCTTAATCCAAATAACTTTGCAAGAGGACTATGAAGATT 180
DB	121	TCGCGCCCTCAGGTCTCTTTCTAAATCCAAATAACTTTGCAAGAGGACTATGAAGATT 180
QY	181	ATGATGAACCTTCTCAAAATATTATGAATTAATGAATACTATTGGGACAGGTGGCTTGC 240
DB	181	ATGATGAACCTTCTCAAAATATTATGAATTAATGAATACTATTGGGACAGGTGGCTTGC 240
QY	241	AGGTCAAACTTGCCTGCCATATCTTACTTGGAGAGATGGTAGCTATAAAATCATGGATA 300
DB	241	AGGTCAAACTTGCCTGCCATATCTTACTTGGAGAGATGGTAGCTATAAAATCATGGATA 300
QY	301	AAACACACTAGGGAGTGAATTTGCCCGGATCAAAACCGAGATTGAGGCTTTGAAGAACC 360
DB	301	AAACACACTAGGGAGTGAATTTGCCCGGATCAAAACCGAGATTGAGGCTTTGAAGAACC 360
QY	361	TGAGACATCAGCATATATGTCAACTCTACCATGTCTAGAGACAGCCAAATAATTCA 420
DB	361	TGAGACATCAGCATATATGTCAACTCTACCATGTCTAGAGACAGCCAAATAATTCA 420
QY	421	TGGTCTTTGAGTACTGCCCTTGAGAGAGAGCTGTGTGACTATATAATTTCCAGGATCGCC 480
DB	421	TGGTCTTTGAGTACTGCCCTTGAGAGAGAGCTGTGTGACTATATAATTTCCAGGATCGCC 480
QY	481	TGTCAGAGAGGAGACCCGGGTGTCTCCGTCAGATAGTATCTGCTGTGTCTTATGTC 540
DB	481	TGTCAGAGAGGAGACCCGGGTGTCTCCGTCAGATAGTATCTGCTGTGTCTTATGTC 540
QY	541	ACAGCCAGGGCTATGCTCAAGGGAACCTCAAGCCAGAAAATTTGCTGTGTGATATATC 600
DB	541	ACAGCCAGGGCTATGCTCAAGGGAACCTCAAGCCAGAAAATTTGCTGTGTGATATATC 600
QY	601	ATAAATTAAGCTGATGATCTTTGGTCTCTGTCGAAACCCCAAGGTAACAGGATTACC 660
DB	601	ATAAATTAAGCTGATGATCTTTGGTCTCTGTCGAAACCCCAAGGTAACAGGATTACC 660
QY	661	ATCTACAGACATGCTGTGGAGTCTGGCTTATGTCAGACACTGAGTTAATACAAAGCAAT 720
DB	661	ATCTACAGACATGCTGTGGAGTCTGGCTTATGTCAGACACTGAGTTAATACAAAGCAAT 720
QY	721	CATATCTTGGATCAGAGCAGATGTTTGGAGCATGGGCATCTGTTATATGTTCTTATGT 780
DB	721	CATATCTTGGATCAGAGCAGATGTTTGGAGCATGGGCATCTGTTATATGTTCTTATGT 780
QY	781	GTGGATTTCTACCATTTGATGATGATGTAATGGCTTATACAGAGAGATTATGAGAG 840
DB	781	GTGGATTTCTACCATTTGATGATGATGTAATGGCTTATACAGAGAGATTATGAGAG 840
QY	841	GAATAATATGATGTTCCCAAGTGGCTCTCTCCAGTAGACATCTGCTTCTTCAACAAATGC 900
DB	841	GAATAATATGATGTTCCCAAGTGGCTCTCTCCAGTAGACATCTGCTTCTTCAACAAATGC 900
QY	901	TGCAGGTGGACCCCAAGAAACCGATTTCTATGAATAATCTATTTGAACCAATCCCTGGATCA 960
DB	901	TGCAGGTGGACCCCAAGAAACCGATTTCTATGAATAATCTATTTGAACCAATCCCTGGATCA 960
QY	961	TGCAAGATTACAACTATCTCTGTTGAGTGGCAAGCAAGAAATCCTTTTATTCACCTCGATG 1020
DB	961	TGCAAGATTACAACTATCTCTGTTGAGTGGCAAGCAAGAAATCCTTTTATTCACCTCGATG 1020


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QY 1021 ATGATTGGCTTAACAGAACTTTCTGTATCATCAAGAAACACAGGCAAAACAATGGAGATT 1080
DB 1021 ATGATTGGCTTAACAGAACTTTCTGTATCATCAAGAAACACAGGCAAAACAATGGAGATT 1080
QY 1081 TAAATTTCACTGTGGCAGTAGATGATCACTCACGGCTACCTATCTTCTGCTTCTAGCCAGA 1140
DB 1081 TAAATTTCACTGTGGCAGTAGATGATCACTCACGGCTACCTATCTTCTGCTTCTAGCCAGA 1140
QY 1141 AGGCTCGGGGAAACACAGTTCGTTTAAAGGCTTTCTTTCTCTCTGTGACCAAGCCAGTG 1200
DB 1141 AGGCTCGGGGAAACACAGTTCGTTTAAAGGCTTTCTTTCTCTCTGTGACCAAGCCAGTG 1200
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DB 1201 CTACCCCATTCACAGACATCAAGTCAAAATAATTTGGAGTCTGGAAGTGAACGCAAGTG 1260
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DB 1321 GTGCTGCTACTCCCGAATCAACAGTTTACCAAGTACTGGACAGAAATCAAAATGGGGTGG 1380
QY 1381 AATCTAAATCAATTAATCTCAGGCTTATGACAGAACACCTGCAAAATAATTTAAAGAACAAAG 1440
DB 1381 AATCTAAATCAATTAATCTCAGGCTTATGACAGAACACCTGCAAAATAATTTAAAGAACAAAG 1440
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DB 1441 AAAATGTATATCTCTTAAGTCTGCTGTAAAGTAAAGAAAGTAAAGTAAAGTAAAGTAAAGT 1500
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QY 1741 CCAAGTGTGGAGCCTTTGAAAGGGGTTGGATAAGGTTATCACTGTGCTCACCAAGGA 1800
DB 1741 CCAAGTGTGGAGCCTTTGAAAGGGGTTGGATAAGGTTATCACTGTGCTCACCAAGGA 1800
QY 1801 GCAGAGGAGGGTTCTGCAGAGACGGGCCAGAGACTTAAGCTTCACTATATGTGA 1860
DB 1801 GCAGAGGAGGGTTCTGCAGAGACGGGCCAGAGACTTAAGCTTCACTATATGTGA 1860
QY 1861 CTACAACTAGATTAGTGAATCCAGATCAACTGTGTAATGAATTAATGTCTATCTTCCAA 1920
DB 1861 CTACAACTAGATTAGTGAATCCAGATCAACTGTGTAATGAATTAATGTCTATCTTCCAA 1920
QY 1921 AGAAGCATGTTGACTTTGTACAAAAGGGTTATACACTGAAGTGTCAACACAGTCAGATT 1980
DB 1921 AGAAGCATGTTGACTTTGTACAAAAGGGTTATACACTGAAGTGTCAACACAGTCAGATT 1980
QY 1981 TTGGGAAAGTGAATGCAATTTGAATTAAGAGTGTGCCAGCTTCAAAAACCCGATGGG 2040
DB 1981 TTGGGAAAGTGAATGCAATTTGAATTAAGAGTGTGCCAGCTTCAAAAACCCGATGGG 2040
QY 2041 TGGGTATCAGGAGGCGCGCTTAAAGGCGATGCTCGGCTTTACAAAAGATTAGTGGAG 2100
DB 2041 TGGGTATCAGGAGGCGCGCTTAAAGGCGATGCTCGGCTTTACAAAAGATTAGTGGAG 2100
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QY 2161 GGTGTGATACAGCTACATATAAGAGCTGTATGATCGCTTTGATTTTAAAGTTTCATTGGAA 2220
DB 2161 GGTGTGATACAGCTACATATAAGAGCTGTATGATCGCTTTGATTTTAAAGTTTCATTGGAA 2220
QY 2221 CTACCAACTTGTTCCTAAAGAGCTATCTTTAAGACCAATATCTCTTTGTTTTTAAACAAA 2280
DB 2221 CTACCAACTTGTTCCTAAAGAGCTATCTTTAAGACCAATATCTCTTTGTTTTTAAACAAA 2280
QY 2281 GATATTTATTTCTGTATGATTAATCAATCAAGCCCATCTGTCAATATGTTACTGTCTTTT 2340
DB 2281 GATATTTATTTCTGTATGATTAATCAATCAAGCCCATCTGTCAATATGTTACTGTCTTTT 2340
QY 2341 TAAATCATGTGGTTTTGTATATTAATAATTTGTTGACTTTCTTAGATTTCACCTCCATATGTG 2400
DB 2341 TAAATCATGTGGTTTTGTATATTAATAATTTGTTGACTTTCTTAGATTTCACCTCCATATGTG 2400
QY 2401 AATGTAAGCTTTAACTATGCTCTCTTTGTAATGTGTAATTTCTTCTGAAATTAACCAT 2460
DB 2401 AATGTAAGCTTTAACTATGCTCTCTTTGTAATGTGTAATTTCTTCTGAAATTAACCAT 2460
QY 2461 TTGTGAATAT 2470
DB 2461 TTGTGAATAT 2470

RESULT 7
ADN39187
ID ADN39187 standard; cDNA; 2470 BP.
XX
AC ADN39187;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:505.
KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnery; gene therapy; vaccine; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003042661-A2.
XX
PD 22-MAY-2003.
XX
PF 13-NOV-2002; 2002WO-US036810.
XX
PR 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-035394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-035250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-039775P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
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XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX Afar D, Ariz N, Gineburg WM, Gish KC, Glynne R, Hevezi PA;
XX Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX WPI; 2003-468649/44.
DR P-PSDB; ADN39188.
XX
PT Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX
PS Claim 8; SEQ ID NO 505; 1385pp; English.
XX
CC The invention relates to nucleic acids and proteins (ADN39683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a nucleic acid sequence of the invention.
XX
XX Sequence 2470 BP; 767 A; 488 C; 536 G; 679 T; 0 U; 0 Other;

Query Match 100.0%; Score 2470; DB 11; Length 2470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGGCGGGGAGCGGCACACCCGGCGATCGAAAGATTCTTAGGAACGCGTACCA 60
DB 1 TTGGCGGGGAGCGGCACACCCGGCGATCGAAAGATTCTTAGGAACGCGTACCA 60
QY 61 GCGCGCTCTCAGGACAGCAGCGCCCTGTCTTCTGTGGGCGCGCTCAGCGCGCC 120
DB 61 GCGCGCTCTCAGGACAGCAGCGCCCTGTCTTCTGTGGGCGCGCTCAGCGCGCC 120
QY 121 TCGCGCCCTCAGGTTCTTTTCTTAATTCCAAATAAACTTGCAAGAGGACTATGAAAGATT 180
DB 121 TCGCGCCCTCAGGTTCTTTTCTTAATTCCAAATAAACTTGCAAGAGGACTATGAAAGATT 180
QY 181 ATGATGAACCTTCAAAATATTATGAATTACATGAACTATTGGACAGGTGGCTTGCAA 240
DB 181 ATGATGAACCTTCAAAATATTATGAATTACATGAACTATTGGACAGGTGGCTTGCAA 240
QY 241 AGGTCAAACTTGCCTGCATATCTTCTTACTGAGAGATGGTAGCTATAAAATCATGCGATA 300
DB 241 AGGTCAAACTTGCCTGCATATCTTCTTACTGAGAGATGGTAGCTATAAAATCATGCGATA 300
QY 301 AAAACACACTAGGAGTGATTTGCCCGGATCAAAAACGAGATTTGAGGCTTGAAGAACC 360
DB 301 AAAACACACTAGGAGTGATTTGCCCGGATCAAAAACGAGATTTGAGGCTTGAAGAACC 360
QY 361 TGAGACATCAGCATATATGTCACTCTACCATGTGTCTAGACAGCCCAAAATATTCA 420
DB 361 TGAGACATCAGCATATATGTCACTCTACCATGTGTCTAGACAGCCCAAAATATTCA 420
QY 421 TGGTCTTGTAGTACTGCCCTGGAGGAGAGCTGTTTGACTATATAATTTCCAGGATCGCC 480
DB 421 TGGTCTTGTAGTACTGCCCTGGAGGAGAGCTGTTTGACTATATAATTTCCAGGATCGCC 480
QY 481 TGTGAGAAGAGGAGACCGCGGTTGTCTTCGGTCAGATAGTATCTGCTGTGTATGTGC 540
DB 481 TGTGAGAAGAGGAGACCGCGGTTGTCTTCGGTCAGATAGTATCTGCTGTGTATGTGC 540

DB 481 TGTGAGAAGAGGAGACCGCGGTTGTCTTCGGTCAGATAGTATCTGCTGTGTATGTGC 540
QY 541 ACAGCAGGGCTATGCTCACAGGGACCTCAAGCCAGAAAAATTTGCTGTTGATGAATATC 600
DB 541 ACAGCAGGGCTATGCTCACAGGGACCTCAAGCCAGAAAAATTTGCTGTTGATGAATATC 600
QY 601 ATAAATTAAGCTGATTGACTTTGTCTCTGTGCAAAACCCCAAGGGTAAACAGGATTACC 660
DB 601 ATAAATTAAGCTGATTGACTTTGTCTCTGTGCAAAACCCCAAGGGTAAACAGGATTACC 660
QY 661 ATCTACAGACATGCTGGGAGTCTGGCTTATGCAAGACCTGAGTTAATACAGGCAAT 720
DB 661 ATCTACAGACATGCTGGGAGTCTGGCTTATGCAAGACCTGAGTTAATACAGGCAAT 720
QY 721 CATATCTTGGATCAGAGGAGATGTTGGAGCATGGGCATCTGTTATATGTTCTTATCT 780
DB 721 CATATCTTGGATCAGAGGAGATGTTGGAGCATGGGCATCTGTTATATGTTCTTATCT 780
QY 781 GTGGATTTCTACCATTTGATGATGATAATGTAATGGCTTTATACAAGAAATATGAGAG 840
DB 781 GTGGATTTCTACCATTTGATGATGATAATGTAATGGCTTTATACAAGAAATATGAGAG 840
QY 841 GAAATATGATGTTCCCAAGTGGCTCTCCCAAGTAGCATCTCTCTTCTTCAACAAATCC 900
DB 841 GAAATATGATGTTCCCAAGTGGCTCTCTCCCAAGTAGCATCTCTCTTCTTCAACAAATCC 900
QY 901 TCGAGTGGACCCAAAGAAACCGATTCTTATGAAAAATCTATTGAACCATCTCTGATCA 960
DB 901 TCGAGTGGACCCAAAGAAACCGATTCTTATGAAAAATCTATTGAACCATCTCTGATCA 960
QY 961 TCGAAGATTACAACATCTCTGTTGAGTGGCAAGCAAGAAATCCTTTTATACCTCGATG 1020
DB 961 TCGAAGATTACAACATCTCTGTTGAGTGGCAAGCAAGAAATCCTTTTATACCTCGATG 1020
QY 1021 ATGATTGGTAAACAGAACTTTCTGTACATCAAGAAACCAAGCAACAAATGAGGATT 1080
DB 1021 ATGATTGGTAAACAGAACTTTCTGTACATCAAGAAACCAAGCAACAAATGAGGATT 1080
QY 1081 TAAATTTCACTGTGGCAGTATGATCACTCACGGCTACCTATCTTCTGTCTTAGCAAGA 1140
DB 1081 TAAATTTCACTGTGGCAGTATGATCACTCACGGCTACCTATCTTCTGTCTTAGCAAGA 1140
QY 1141 AGGCTCGGGGAAAAACAGTTTCGTTTAAAGGCTTTCTTTCTCTCTGTGCAAGCCAGTG 1200
DB 1141 AGGCTCGGGGAAAAACAGTTTCGTTTAAAGGCTTTCTTTCTCTCTGTGCAAGCCAGTG 1200
QY 1201 CTACCCCATTCACAGACATCAAGTCAATTAATTTGGAGTCTGGAAGATGACCGCAAGTG 1260
DB 1201 CTACCCCATTCACAGACATCAAGTCAATTAATTTGGAGTCTGGAAGATGACCGCAAGTG 1260
QY 1261 ATAAAAATTTATGTGGCGGATTAATAGACTATGATTTGGTGTGAAGATGATTTATCAACAG 1320
DB 1261 ATAAAAATTTATGTGGCGGATTAATAGACTATGATTTGGTGTGAAGATGATTTATCAACAG 1320
QY 1321 GTGCTGCTACTCCCCGAACATCAGAGTTTAAACAGTACTGGAAGATCAAAATGAGGTTG 1380
DB 1321 GTGCTGCTACTCCCCGAACATCAGAGTTTAAACAGTACTGGAAGATCAAAATGAGGTTG 1380
QY 1381 AATCTAAATCATTAATCTCAGCTTATGCAAGAACCTCTGCAAAATTAATTAAGAAACAAAG 1440
DB 1381 AATCTAAATCATTAATCTCAGCTTATGCAAGAACCTCTGCAAAATTAATTAAGAAACAAAG 1440
QY 1441 AAAATGTATATACTCTTAAGTCTGTGTAAGAAATGAAGAGTACTTTATGTTTCTTGAGC 1500
DB 1441 AAAATGTATATACTCTTAAGTCTGTGTAAGAAATGAAGAGTACTTTATGTTTCTTGAGC 1500
QY 1501 CAAAGACTCCAGTTAATAAGAACCCAGCATTAAGAGAGAAATACTCTACTAGCCCAATCGTT 1560
DB 1501 CAAAGACTCCAGTTAATAAGAACCCAGCATTAAGAGAGAAATACTCTACTAGCCCAATCGTT 1560
QY 1561 ACCTACACCTCAAAAGCTAGAAACCCAGTCTGAAAGAACTCCAAATTAATTAATACCAG 1620
DB 1561 ACCTACACCTCAAAAGCTAGAAACCCAGTCTGAAAGAACTCCAAATTAATTAATACCAG 1620

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QY 1621 TAAATTCACAGGACAGACAGCTTAATGACAGGTGTCTATTAGCCCTGAGAGCGGTGCC 1680
Db 1621 TAAATTCACAGGACAGACAGCTTAATGACAGGTGTCTATTAGCCCTGAGAGCGGTGCC 1680
QY 1681 GCTCAGTGGAAATTTGGATCTCAACACAGCACATATGGAGGAGACTCCAAAAAGAAAGGGAG 1740
Db 1681 GCTCAGTGGAAATTTGGATCTCAACACAGCACATATGGAGGAGACTCCAAAAAGAAAGGGAG 1740
QY 1741 CCAAAGTGTGGAGAGCTTTGAAAGGGGTTGGATAAGGTTATCACTGTGCTCACCAGGA 1800
Db 1741 CCAAAGTGTGGAGAGCTTTGAAAGGGGTTGGATAAGGTTATCACTGTGCTCACCAGGA 1800
QY 1801 GCAAAAGGAGGGTCTGCCAGAGACGGGCCCAAGAGACTTAAAGCTTCACTATAATGTGA 1860
Db 1801 GCAAAAGGAGGGTCTGCCAGAGACGGGCCCAAGAGACTTAAAGCTTCACTATAATGTGA 1860
QY 1861 CTACAACTAGATTAGTGAATCCAGATCAACTGTTGAATGAATAAATGTCTATTCTCCAA 1920
Db 1861 CTACAACTAGATTAGTGAATCCAGATCAACTGTTGAATGAATAAATGTCTATTCTCCAA 1920
QY 1921 AGAAGCATGTGTGCTTTGTACAAAAGGGTTATACACTGAAGTGTCAAAACACAGTCAGATT 1980
Db 1921 AGAAGCATGTGTGCTTTGTACAAAAGGGTTATACACTGAAGTGTCAAAACACAGTCAGATT 1980
QY 1981 TTGGGAAAGTGACATGCAATTTGAATTTAGAAAGTGTGCCAGCTTCAAAAACCCGATGTGG 2040
Db 1981 TTGGGAAAGTGACATGCAATTTGAATTTAGAAAGTGTGCCAGCTTCAAAAACCCGATGTGG 2040
QY 2041 TGGGTATCAGGAGCGAGCGCTTAAAGCGGATGCTCCCTGGGTTTACAAAAGATTAGTGGAG 2100
Db 2041 TGGGTATCAGGAGCGAGCGCTTAAAGCGGATGCTCCCTGGGTTTACAAAAGATTAGTGGAG 2100
QY 2101 ACATCCTATCTAGCTGCAAGGTATAATGATGGATTCTTCCATCTCCGCGGATGAGTGTG 2160
Db 2101 ACATCCTATCTAGCTGCAAGGTATAATGATGGATTCTTCCATCTCCGCGGATGAGTGTG 2160
QY 2161 GGTGTGATACAGCTACATAAGACCTGTATGATGCTTTGATGCTTTTAAAGTTCAATTGGAA 2220
Db 2161 GGTGTGATACAGCTACATAAGACCTGTATGATGCTTTGATGCTTTTAAAGTTCAATTGGAA 2220
QY 2221 CTACCAACTTGTCTTAAAGAGCTATCTTAAAGACCAATATCTCTTGTGTTTTTAAACAAA 2280
Db 2221 CTACCAACTTGTCTTAAAGAGCTATCTTAAAGACCAATATCTCTTGTGTTTTTAAACAAA 2280
QY 2281 GATATTATTTGTGTATGAATCTAAATCAAGCCCATCTGTCAATTATGTTACTGTCTTTT 2340
Db 2281 GATATTATTTGTGTATGAATCTAAATCAAGCCCATCTGTCAATTATGTTACTGTCTTTT 2340
QY 2341 TAATCATGTGTTTGTATTAATAATTTGTTGACTTTCTTAGATTCACTTCCATATGTG 2400
Db 2341 TAATCATGTGTTTGTATTAATAATTTGTTGACTTTCTTAGATTCACTTCCATATGTG 2400
QY 2401 AATGTAAGCTCTTAACATGCTCTTTGTAATGTGTAATTTCTTCTGTAATAAACCAT 2460
Db 2401 AATGTAAGCTCTTAACATGCTCTTTGTAATGTGTAATTTCTTCTGTAATAAACCAT 2460
QY 2461 TTGTGAATAT 2470
Db 2461 TTGTGAATAT 2470
```

RESULT 8
ADM72650

ID ADM72650 standard; cDNA; 2470 BP.

XX AC ADM72650;

XX DT 17-JUN-2004 (first entry)

XX DE Human TASK110 polypeptide encoding cDNA (clone DNA255289).

XX KW TASK; tumour-associated kinase; cytostatic; tumour;

KW cell proliferative disorder; cancer; transgenic; chromosome identification; tissue typing; human; TASK110; gene; ss.
XX Homo sapiens.

Key Location/Qualifiers
CDS 171..2126
/*tag= a
/product= "TASK110"

W02004024063-A2.

25-MAR-2004.

05-SEP-2003; 2003WO-US027886.

11-SEP-2002; 2002US-0410166P.

(GETH) GENENTECH INC.

Davis DP, Desauvage FJ, Wood WI, Zhang Z;

WPI: 2004-282984/26.

P-PSDB; ADM72651.

New tumor-associated kinase nucleic acids and polypeptides, useful as hybridization probes for isolating full length TASK DNA, for generating transgenic animals, in chromosome identification, or for tissue typing.

Claim 1; Fig 1; 140pp; English.

The invention relates to tumour-associated kinase (TASK) polypeptides (II) and encoding polynucleotides. An antibody, oligopeptide (siRNA) or organic molecule that binds to (II) is useful for treating a mammal having a tumour comprising cells expressing (II). Antagonists of TASK are useful for treating or preventing a cell proliferative disorder (e.g. cancer) associated with increased expression or activity of (II). The TASK polynucleotides and polypeptides may be used as hybridization probes for isolating full length TASK DNA, for generating transgenic animals, in chromosome identification, or for tissue typing. The present sequence represents a cDNA encoding a human TASK110 polypeptide.

Sequence 2470 BP; 767 A; 488 C; 536 G; 679 T; 0 U; 0 Other;

Query Match 100.0%; Score 2470; DB 12; Length 2470;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCGGGCGGAAGCGGCCACAAACCGCGGATCGAAAAGATTCTTAGGAACCGCGTACCA 60

Db 1 TTGGCGGGCGGAAGCGGCCACAAACCGCGGATCGAAAAGATTCTTAGGAACCGCGTACCA 60

QY 61 GCCGGTCTCTCAGACACAGCGGCCCTGTCTCTGTGGCGCGCGCTCAGCCGTGCC 120

Db 61 GCCGGTCTCTCAGACACAGCGGCCCTGTCTCTGTGGCGCGCGCTCAGCCGTGCC 120

QY 121 TCCGCCCTCTCAGGTCTCTTTTCTTAATTCAAATAAATTGCAAGAGGACTATGAAGATT 180

Db 121 TCCGCCCTCTCAGGTCTCTTTTCTTAATTCAAATAAATTGCAAGAGGACTATGAAGATT 180

QY 181 ATGATGAATCTTCAATATTAATGAATTAATGAATTAATGGGACAGGTGCTTTGCAA 240

Db 181 ATGATGAATCTTCAATATTAATGAATTAATGAATTAATGGGACAGGTGCTTTGCAA 240

QY 241 AGGTCAAACTTGCCTGCCATATCTTACTGGAGAGATGTAGCTATAAAATCATGGATA 300

Db 241 AGGTCAAACTTGCCTGCCATATCTTACTGGAGAGATGTAGCTATAAAATCATGGATA 300

QY 301 AAAACACACTAGGGAGTGAATTTGCCCGGATCAAAACCGAGATTGAGGCTTTGAAGAACC 360

Db 301 AAAACACACTAGGGAGTGAATTTGCCCGGATCAAAACCGAGATTGAGGCTTTGAAGAACC 360

QY 361 TGAGACATAGCATATATGTCAACTCTTACCATGTCTAGAGACAGCCAAATAATTCA 420

[illegible]

1441	DB	AAATGTATATATCTCCTAAGTCTGTGTTAAAGATGAAGAGTACTTTATGTGTTCTCTGAGC	1500
1501	QY	CAAGAAGCTCCAGTTAATAAGAAACCAAGCATAAAGAGAAATACTCACTAGCCCAAAATCGTT	1560
1501	DB	CAAAGACTCCAGTTAATAGAACCAAGCATAAAGAGAAATACTCACTAGCCCAAAATCGTT	1560
1561	QY	ACACTACACCTTCAAAGCTTAGAAAACAGTGCCTGAAAAGAACTCCAAATTTAAATATACCAG	1620
1561	DB	ACACTACACCTTCAAAGCTTAGAAAACAGTGCCTGAAAAGAACTCCAAATTTAAATATACCAG	1620
1621	QY	TAAATTTCAACAGAAACAGACAGTAAATGACAGGTCTCATTTAGCCCTGAGAGCGCGTGCC	1680
1621	DB	TAAATTTCAACAGAAACAGACAGTAAATGACAGGTCTCATTTAGCCCTGAGAGCGCGTGCC	1680
1681	QY	GCTCAGTGGAAATTTGGATCTTCAACCAAGACACATATGAGGAGAGACTCCAAAAGAAAGGGAG	1740
1681	DB	GCTCAGTGGAAATTTGGATCTTCAACCAAGACACATATGAGGAGAGACTCCAAAAGAAAGGGAG	1740
1741	QY	CCAAAGTGTGTTGGAGGCCCTTGAAGGGGTTGGATAAGGTTATCACTGTGCTCACACAGGA	1800
1741	DB	CCAAAGTGTGTTGGAGGCCCTTGAAGGGGTTGGATAAGGTTATCACTGTGCTCACACAGGA	1800
1801	QY	GCAAAAGGAGGGTCTTGCCAGAGAGCGGCCCCAGABAGACTTAAGCTTCACTATAATGTGA	1860
1801	DB	GCAAAAGGAGGGTCTTGCCAGAGAGCGGCCCCAGABAGACTTAAGCTTCACTATAATGTGA	1860
1861	QY	CTCAACTAGATTAAGTGAATCCAGATCAACTGTTTGAATGAAATAAATGTCTATTCTTCCAA	1920
1861	DB	CTCAACTAGATTAAGTGAATCCAGATCAACTGTTTGAATGAAATAAATGTCTATTCTTCCAA	1920
1921	QY	AGAAGCATGTTGACTTTTGTAACAAAAGGGTTATACA CTGAAGTGTCAAAACACAGTCAGATT	1980
1921	DB	AGAAGCATGTTGACTTTTGTAACAAAAGGGTTATACA CTGAAGTGTCAAAACACAGTCAGATT	1980
1981	QY	TTGGGAAAGTGACAAATGCAATTTGAATTAAGAAGTGTGCCAGCTTCAAAAACCCGATGTGG	2040
1981	DB	TTGGGAAAGTGACAAATGCAATTTGAATTAAGAAGTGTGCCAGCTTCAAAAACCCGATGTGG	2040
2041	QY	TGGGTATCAGAGGCGAGCGGCTTTAAGGGCGATGCCCTGGGTTTACAAAAGATTAGTGGAAAG	2100
2041	DB	TGGGTATCAGAGGCGAGCGGCTTTAAGGGCGATGCCCTGGGTTTACAAAAGATTAGTGGAAAG	2100
2101	QY	ACATCCTATCTAGCTGCAAGGTATAATTGATGGAATCTTCCATCCTGCCGGATGAGTGTG	2160
2101	DB	ACATCCTATCTAGCTGCAAGGTATAATTGATGGAATCTTCCATCCTGCCGGATGAGTGTG	2160
2161	QY	GGTGTGATACAGCCTACATAAAGACTGTTATGATCGCTTTGATTTTAAAGTTCATTTGGAA	2220
2161	DB	GGTGTGATACAGCCTACATAAAGACTGTTATGATCGCTTTGATTTTAAAGTTCATTTGGAA	2220
2221	QY	CTACCAACTTGTCTTAAAGAGCTATCTTAAGACCAATATCTCTTGTGTTTTTAAACAAA	2280
2221	DB	CTACCAACTTGTCTTAAAGAGCTATCTTAAGACCAATATCTCTTGTGTTTTTAAACAAA	2280
2281	QY	GATATTATTGTTGATGAATCTPAAATCAAGCCCATCTGTCAATATGTTACTGTCTTTTT	2340
2281	DB	GATATTATTGTTGATGAATCTPAAATCAAGCCCATCTGTCAATATGTTACTGTCTTTTT	2340
2341	QY	TAATCATGTGGTTTTGTATATTAATAATTTGTGTGACTTCTTAGATTCACCTCCCATATGTC	2400
2341	DB	TAATCATGTGGTTTTGTATATTAATAATTTGTGTGACTTCTTAGATTCACCTCCCATATGTC	2400
2401	QY	AAATGTAAGCTCTTAACTATGCTCTTTGTAATGTGAATTTCTTTCTGAAATAAAACCAT	2460
2401	DB	AAATGTAAGCTCTTAACTATGCTCTTTGTAATGTGAATTTCTTTCTGAAATAAAACCAT	2460
2461	QY	TTGTGAATAT 2470	
2461	DB	TTGTGAATAT 2470	
RESULT 9			
ADMT2216			

ID ADW72216 standard; cDNA; 2470 BP.
 AC ADW72216;
 DT 17-JUN-2004 (first entry)
 DE Human TASK110 polypeptide encoding cDNA (clone Id DNA255289).
 XX
 KW TASK; tumour-associated kinase; cytostatic; tumour antigen;
 KW cell proliferative disorder; cancer; transgenic; human; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 171..2126
 FT /*tag= a
 FT /product= "TASK110"
 XX
 PN WO2004024064-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 05-SEP-2003; 2003WO-US027894.
 XX
 PR 11-SEP-2002; 2002US-0410166P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Desauvage FJ, Wood WI, Zhang Z;
 XX
 DR WPI; 2004-282985/26.
 DR P-PSDB; ADW72217.
 XX
 XX New tumor-associated kinase nucleic acids and polypeptides, useful as
 PT hybridization probes for isolating full length TASK DNA, for generating
 PT transgenic animals, in chromosome identification, or for tissue typing.
 XX
 PS Claim 2; SEQ ID NO 21; 163pp; English.
 XX
 CC The invention relates to new isolated tumour-associated kinase (TASK)
 CC nucleic acid molecules and encoded polypeptides. Cytostatic. The
 CC antibody, oligopeptide or organic molecule that binds to the TASK
 CC polypeptide are useful for treating a mammal having a tumour comprising
 CC cells expressing the polypeptide. Antagonists of TASK are useful for
 CC treating or preventing a cell proliferative disorder (e.g. cancer)
 CC associated with increased expression or activity of TASK polypeptide. The
 CC TASK polynucleotides and polypeptides may be used as hybridization probes
 CC for isolating full length TASK DNA, for generating transgenic animals, in
 CC chromosome identification, or for tissue typing. The present sequence
 CC represents a cDNA encoding a human TASK polypeptide.
 XX
 SQ Sequence 2470 BP; 767 A; 488 C; 536 G; 679 T; 0 U; 0 Other;
 Query Match 100.0%; Score 2470; DB 12; Length 2470;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTGGGGGGGGGAGCGGCCACAAACCGCGGATCGAAAGATTCTTAGGAAACCGCGTACCA 60
 DB 1 TTGGGGGGGGGAGCGGCCACAAACCGCGGATCGAAAGATTCTTAGGAAACCGCGTACCA 60
 QY 61 GCCGGCTCTCTCAGGACACAGCGGCCCTCTCTCTCTGTCGGCGCGCTCAGCCGTCGCC 120
 DB 61 GCCGGCTCTCTCAGGACACAGCGGCCCTCTCTCTCTGTCGGCGCGCTCAGCCGTCGCC 120
 QY 121 TCGGCCCTCAGGTTCTTTTCTTAATTCAAATAAATTGCAAGAGACTATGAAGATT 180
 DB 121 TCGGCCCTCAGGTTCTTTTCTTAATTCAAATAAATTGCAAGAGACTATGAAGATT 180
 QY 181 ATGATGAACCTCTCAAAATTAATGAATACATGAACATTAATTCGGACAGTGGCTTTGCAA 240
 DB 181 ATGATGAACCTCTCAAAATTAATGAATACATGAACATTAATTCGGACAGTGGCTTTGCAA 240

QY 241 AGGTCAAACTTGCCTGCCATATCCTTACTGGAGAGATGGTAGCTATAAAAAATCATGGATA 300
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 DB 241 AGGTCAAACTTGCCTGCCATATCCTTACTGGAGAGATGGTAGCTATAAAAAATCATGGATA 300
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 DB |||||
 DB 301 AAAACACACTAGGAGTGAATTTGCCCGGATCAAAACGGAGATTGAGGCTTTGGAAGACC 360
 QY 361 TGAGACATCAGCATATATGTCAACTCTACCATGTCTAGAGACAGCAACAAAATATTCA 420
 DB |||||
 DB 361 TGAGACATCAGCATATATGTCAACTCTACCATGTCTAGAGACAGCAACAAAATATTCA 420
 QY 421 TGGTTCTTGAGTACTGCCCTCGAGGAGAGCTGTTTGA CTATATAATTTCCAGGATCGCC 480
 DB |||||
 DB 421 TGGTTCTTGAGTACTGCCCTCGAGGAGAGCTGTTTGA CTATATAATTTCCAGGATCGCC 480
 QY 481 TGTCAAGAGAGAGACCCGGGTTGCTTCCTCGTACAGTATCTGCTGTGCTTATGTCG 540
 DB |||||
 DB 481 TGTCAAGAGAGAGACCCGGGTTGCTTCCTCGTACAGTATCTGCTGTGCTTATGTCG 540
 QY 541 ACAGCCAGGGCTATGCTCA CAGGACCTCAAGCCAGAAAATTTGCTGTTTGTATGAATATC 600
 DB |||||
 DB 541 ACAGCCAGGGCTATGCTCA CAGGACCTCAAGCCAGAAAATTTGCTGTTTGTATGAATATC 600
 QY 601 ATAAATTAAGCTGATGACTTTTGGTCTCTGTGCAAAACCCAAAGGTAAACAGGATTACC 660
 DB |||||
 DB 601 ATAAATTAAGCTGATGACTTTTGGTCTCTGTGCAAAACCCAAAGGTAAACAGGATTACC 660
 QY 661 ATCTACAGACATGCTGTGGAGTCTGGCTTATGCAAGACCTGAGTTAATACAGGCAAT 720
 DB |||||
 DB 661 ATCTACAGACATGCTGTGGAGTCTGGCTTATGCAAGACCTGAGTTAATACAGGCAAT 720
 QY 721 CATATCTTGGATCAGAGCAGATGTTGGAGCATGGGCATCTGTTATATGTTCTTATGCT 780
 DB |||||
 DB 721 CATATCTTGGATCAGAGCAGATGTTGGAGCATGGGCATCTGTTATATGTTCTTATGCT 780
 QY 781 GTGGATTTCTACCATTTGATGATTAATGTAATGGCTTTATACAAAGAGATTATGAGAG 840
 DB |||||
 DB 781 GTGGATTTCTACCATTTGATGATTAATGTAATGGCTTTATACAAAGAGATTATGAGAG 840
 QY 841 GAAATATGATGTTCCCAAGTGGCTCTCCAGTAGCATCTGCTTCTTCAACAAATGC 900
 DB |||||
 DB 841 GAAATATGATGTTCCCAAGTGGCTCTCTCCAGTAGCATCTGCTTCTTCAACAAATGC 900
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 DB |||||
 DB 901 TGCAGGTGGAACCAAGAAACCGATTCTTATGAAAATCTATTGAACCATCCTCGATCA 960
 QY 961 TGAAGATTACAACTATCTGTTGAGTGGCAAGCAAGATCCTTTTATTCACCTCGATG 1020
 DB |||||
 DB 961 TGAAGATTACAACTATCTGTTGAGTGGCAAGCAAGATCCTTTTATTCACCTCGATG 1020
 QY 1021 ATGATTTGCTAACGAACTTTCTGTACATCA CAGAAACCAAGCAACATGGAGGATT 1080
 DB |||||
 DB 1021 ATGATTTGCTAACGAACTTTCTGTACATCA CAGAAACCAAGCAACATGGAGGATT 1080
 QY 1081 TAAATTTCACTGTGGCAGTATGATCACTCA CGGCTACCTATCTTCTGTCTTAGCAAGA 1140
 DB |||||
 DB 1081 TAAATTTCACTGTGGCAGTATGATCACTCA CGGCTACCTATCTTCTGTCTTAGCAAGA 1140
 QY 1141 AGGCTCGGGGAAAACCAAGTCTGTTTAAAGCTTTCTTTCTCTGTGTGGAAGAAGCAGTG 1200
 DB |||||
 DB 1141 AGGCTCGGGGAAAACCAAGTCTGTTTAAAGCTTTCTTTCTCTGTGTGGAAGAAGCAGTG 1200
 QY 1201 CTACCCCAATTCAGACATCAAGTCAAAATATGGAGTCTGGAAGATGTCGCCGCAAGTG 1260
 DB |||||
 DB 1201 CTACCCCAATTCAGACATCAAGTCAAAATATGGAGTCTGGAAGATGTCGCCGCAAGTG 1260
 QY 1261 ATAAAAATTTATGTGGCGGATTAATAGACTATGATTTGGTGTGAAGATGATTTATCAACAG 1320
 DB |||||
 DB 1261 ATAAAAATTTATGTGGCGGATTAATAGACTATGATTTGGTGTGAAGATGATTTATCAACAG 1320
 QY 1321 GTGCTGCTACTCCCGCAACATCACAGTTTACAAGTACTGGACAGAAATCAAAATGGGGTGG 1380

1321 GTGCTGCTACTCCCGCAACATCACAGCTTTACCAAGTACTGGACAGAAATCAAAATGGGGTGG 1380
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1381 AATCTTAANTCATTAATCCAGCCTTATGAGACACCTCCAAATAAATTAAGAACAAG 1440
1441 AAAATGTATATCTCTCTAGTCTGTGTAAGAAATGAAGTACTTTATATGTTCTCTGAGC 1500
1441 AAAATGTATATCTCTCTAGTCTGTGTAAGAAATGAAGTACTTTATATGTTCTCTGAGC 1500
1501 CAAAGACTCCAGTTAATAAGAACCCAGCATAGAGAGAAATATCTCATAGCCCAAAATCGTT 1560
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1561 ACATACACCTCAAAAGCTAGAAACCCAGTCCCTGAAAGAACTCAATTAATAATACAG 1620
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1621 TAAATTTCAACAGGACAGACAAGTTAATGACAGGTGTCTATTAGCCTGAGAGCGGTGCC 1680
1681 GCTCAGTGGAAATGGATCTCAACCAAGCACATATGAGGAGACTCCAAAAGAAAGGGAG 1740
1681 GCTCAGTGGAAATGGATCTCAACCAAGCACATATGAGGAGACTCCAAAAGAAAGGGAG 1740
1741 CCAAAGTGTGGAGCCTTGAAGGGGGTGGATAAGGTATACCTGTGCTCACCAGGA 1800
1741 CCAAAGTGTGGAGCCTTGAAGGGGGTGGATAAGGTATACCTGTGCTCACCAGGA 1800
1801 GCAAAAGGAGGGTCTGCGCAGAGACGGGCCAGAGACTTAAAGCTTCACTATAATGTGA 1860
1801 GCAAAAGGAGGGTCTGCGCAGAGACGGGCCAGAGACTTAAAGCTTCACTATAATGTGA 1860
1861 CTA CAAC TAGATTAGTGAATCCAGATCAACTGTGTTGAATGAATAATGTCTATTTCCAA 1920
1861 CTA CAAC TAGATTAGTGAATCCAGATCAACTGTGTTGAATGAATAATGTCTATTTCCAA 1920
1921 AGAAGCATGTTGATCTTTGTACAAAGGGTTATACAGTGTCAAGTGTCAACACAGTCAAGT 1980
1921 AGAAGCATGTTGATCTTTGTACAAAGGGTTATACAGTGTCAAGTGTCAACACAGTCAAGT 1980
1981 TTGGGAAAGTGACAATGCAATTTGAATTAGAAGTGTGCCAGCTTCAAAAACCGGATGTGG 2040
1981 TTGGGAAAGTGACAATGCAATTTGAATTAGAAGTGTGCCAGCTTCAAAAACCGGATGTGG 2040
2041 TGGGTATCAGGAGCGCGCTTAAAGGCGATGCCCTGGGTTTACAAAAGATTAGTGGAA 2100
2041 TGGGTATCAGGAGCGCGCTTAAAGGCGATGCCCTGGGTTTACAAAAGATTAGTGGAA 2100
2101 ACATCTATCTAGCTGCAAGGTATTAATGATGATTTCTTCATCTCCATCCCTGCGGATGTGG 2160
2101 ACATCTATCTAGCTGCAAGGTATTAATGATGATTTCTTCATCTCCATCCCTGCGGATGTGG 2160
2161 GGTGTGATACAGCTCATATAAGACTGTTATGATCGCTTTGATTTTAAAGTTCATTGGAA 2220
2161 GGTGTGATACAGCTCATATAAGACTGTTATGATCGCTTTGATTTTAAAGTTCATTGGAA 2220
2221 CTA CCAACTTTGTTTCTAAAGAGCTATCTTAAGACCAATATCTCTTTGTTTTTAAACAAA 2280
2221 CTA CCAACTTTGTTTCTAAAGAGCTATCTTAAGACCAATATCTCTTTGTTTTTAAACAAA 2280
2281 GATATATTTTGTATGATTAATTAATCAAGCCCATCTGTCATATGTTACTGCTTTTTT 2340
2281 GATATATTTTGTATGATTAATTAATCAAGCCCATCTGTCATATGTTACTGCTTTTTT 2340
2341 TAATCATGTGTTTGTATATTAATTAATTTGATCTTTCTAGATTTCTTACATTTCCATATGTG 2400
2341 TAATCATGTGTTTGTATATTAATTAATTTGATCTTTCTAGATTTCTTACATTTCCATATGTG 2400
2401 AATGTAAGCTCTTAACATATCTCTTTTGAATGTGAATTTCTTTCTGAAATAAACCAT 2460

2401 AATGTAAGCTCTTAACATATCTCTTTTGAATGTGAATTTCTTTCTGAAATAAACCAT 2460
2461 TTGTGAATAT 2470
2461 TTGTGAATAT 2470
2461 TTGTGAATAT 2470
RESULT 10
ADN06035
ID ADN06035 standard; cDNA; 2470 BP.
XX
AC ADN06035;
XX
DT 01-JUL-2004 (first entry)
XX
DE Antipsoriatic cDNA sequence #1256.
XX
KW ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
XX
OS Homo sapiens.
XX
PN WO2004028479-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030907.
XX
PR 25-SEP-2002; 2002US-0414006P.
XX
PA (GETH) GENENTECH INC.
XX
PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;
XX
DR WPI; 2004-305105/28.
XX
P-PSDB; ADN06036.
PT New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX
PS Claim 1; SEQ ID NO 2430; 3069pp; English.
XX
CC The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polynucleotides of the invention.
XX
SQ Sequence 2470 BP; 767 A; 488 C; 536 G; 679 T; 0 U; 0 Other;
Query Match 100.0%; Score 2470; DB 12; Length 2470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGGGGGGGGGAGGGGGCCACCAACCGGCGATCGAAAGATTCTTAGGAACGCCGTACCA 60
DB 1 TTGGGGGGGGGAGGGGGCCACCAACCGGCGATCGAAAGATTCTTAGGAACGCCGTACCA 60
QY 61 GCGCGCTCTCTCAGACACAGCGCCCTCTCTTCTGTGCGGGCGCGCTCAGCCGTGCC 120
DB 61 GCGCGCTCTCTCAGACACAGCGCCCTCTCTTCTGTGCGGGCGCGCTCAGCCGTGCC 120
QY 121 TCGCCCCCTCAGTCTCTTTTCTTAATTCCAAATAAATTGCAAGAGACTATGAAAAGATT 180
DB 121 TCGCCCCCTCAGTCTCTTTTCTTAATTCCAAATAAATTGCAAGAGACTATGAAAAGATT 180
QY 181 ATGATGAACCTCTCAAATATTATGAATACATGAACTATTGGAACAGACTATGAAAGATT 240
DB 181 ATGATGAACCTCTCAAATATTATGAATACATGAACTATTGGAACAGACTATGAAAGATT 240
QY 241 AGGTCAAACCTGCTGCCATATCTTACTGGAGAGATGTTAGTATAAATCATCATGATA 300

Db 241 AGGTCAAACTTGCTGCTATATCTTACTGGAGAGATGGTAGCTATAAAAAATCATGGATA 300
Qy 301 AAAACACATAGGAGATGATTTGCCCGGATCAAAAACGAGATGTAGGCGCTTGAAGAACC 360
Db 301 AAAACACATAGGAGATGATTTGCCCGGATCAAAAACGAGATGTAGGCGCTTGAAGAACC 360
Qy 361 TGAGACATCAGCATATATGTCAACTCTACCATGTGCTAGAGACAGCAACAATAATTC 420
Db 361 TGAGACATCAGCATATATGTCAACTCTACCATGTGCTAGAGACAGCAACAATAATTC 420
Qy 421 TGGTTCTTGAGTACTGCCCTGGAGGAGAGCTGTTTGACTATATAAATTTCCAGGATCGCC 480
Db 421 TGGTTCTTGAGTACTGCCCTGGAGGAGAGCTGTTTGACTATATAAATTTCCAGGATCGCC 480
Qy 481 TGTCAAGAAGGAGAGACCGGGTTGTCTTCGTCAGATAGTATCTGCTGTGTTTATGTGC 540
Db 481 TGTCAAGAAGGAGAGACCGGGTTGTCTTCGTCAGATAGTATCTGCTGTGTTTATGTGC 540
Qy 541 ACAGCCAGGGCTATGCTCAAGGGAGCTCAAGCCAGAAAATTTGGCTGTTTGATGAATATC 600
Db 541 ACAGCCAGGGCTATGCTCAAGGGAGCTCAAGCCAGAAAATTTGGCTGTTTGATGAATATC 600
Qy 601 ATAAATTAAGCTGATTTGACTTTGGTCTCTGTGCAAAAACCAAGGGTAAACAAGGATTAAC 660
Db 601 ATAAATTAAGCTGATTTGACTTTGGTCTCTGTGCAAAAACCAAGGGTAAACAAGGATTAAC 660
Qy 661 ATCTACAGACATGCTGTGGAGGCTCGGCTTATGACACACCTGAGTTAAATACAAGGCAAT 720
Db 661 ATCTACAGACATGCTGTGGAGGCTCGGCTTATGACACACCTGAGTTAAATACAAGGCAAT 720
Qy 721 CATATCTTGGATCAGAGGAGATGTTTGGAGCATGCGCATCTGTTATATGTTCTTATGT 780
Db 721 CATATCTTGGATCAGAGGAGATGTTTGGAGCATGCGCATCTGTTATATGTTCTTATGT 780
Qy 781 GTGGATTTCTACCATTTGATGATGATAATGTAATGGCTTTATACAGAAGATTTATGAGAG 840
Db 781 GTGGATTTCTACCATTTGATGATGATAATGTAATGGCTTTATACAGAAGATTTATGAGAG 840
Qy 841 GAAAATATGATGTTCCAAAGTGCTCTCCCAAGTAGCATCTGCTTCTTCAACAAATGC 900
Db 841 GAAAATATGATGTTCCAAAGTGCTCTCCCAAGTAGCATCTGCTTCTTCAACAAATGC 900
Qy 901 TGCAGGTGACCCAAAGAACGGATTTCTATGAAAATCTATGAAACCTATGAAACCTCCGTGATCA 960
Db 901 TGCAGGTGACCCAAAGAACGGATTTCTATGAAAATCTATGAAACCTATGAAACCTCCGTGATCA 960
Qy 961 TGCAGATTAACAATCTATCTGTTGAGTGGCAAGCAAGATCCTTTTATTCACCTCGATG 1020
Db 961 TGCAGATTAACAATCTATCTGTTGAGTGGCAAGCAAGATCCTTTTATTCACCTCGATG 1020
Qy 1021 ATGATTTGGTAAACAGAACTTTCTGTATCATCAGAAAACACAGGCAAAACAATGGAGGATT 1080
Db 1021 ATGATTTGGTAAACAGAACTTTCTGTATCATCAGAAAACACAGGCAAAACAATGGAGGATT 1080
Qy 1081 TAAATTTCACTGGCGAGTATGATACCTCACGGCTACCTATCTTCTGCTTCTAGCCAAAGA 1140
Db 1081 TAAATTTCACTGGCGAGTATGATACCTCACGGCTACCTATCTTCTGCTTCTAGCCAAAGA 1140
Qy 1141 AGGCTCGGGGAAAACAGTTTCTTTAAGGCTTTCTTTCTTCTGTTGAGCAAGCCAGTG 1200
Db 1141 AGGCTCGGGGAAAACAGTTTCTTTAAGGCTTTCTTTCTTCTGTTGAGCAAGCCAGTG 1200
Qy 1201 CTACCCCAATTCACAGATCAAGTCAAAATAATGGAGTCTGGAAGATGTGACCGCAAGTG 1260
Db 1201 CTACCCCAATTCACAGATCAAGTCAAAATAATGGAGTCTGGAAGATGTGACCGCAAGTG 1260
Qy 1261 ATAAAAATATGTGGCGGATTAATAGACTATGATTTGGTGAAGATGATTTATCAACAG 1320
Db 1261 ATAAAAATATGTGGCGGATTAATAGACTATGATTTGGTGAAGATGATTTATCAACAG 1320
Qy 1321 GTGCTGTACTCCCGAATCATCAGATTTTACCAAGTCTGGACAGAAATCAATGGGGTGG 1380
Db 1321 GTGCTGTACTCCCGAATCATCAGATTTTACCAAGTCTGGACAGAAATCAATGGGGTGG 1380

Qy 1381 AATCTAAATCATTAATCTCAGGCTTATGAGAACACCTCCAAATAAATTAAGAAACAAG 1440
Db 1381 AATCTAAATCATTAATCTCAGGCTTATGAGAACACCTCCAAATAAATTAAGAAACAAG 1440
Qy 1441 AAAATGTATATCTCCTTAAGTCTGCTGTAAGAAAGTAAGAGTACTTTATGTTTCTGAGC 1500
Db 1441 AAAATGTATATCTCCTTAAGTCTGCTGTAAGAAAGTAAGAGTACTTTATGTTTCTGAGC 1500
Qy 1501 CAAAGACTCCAGTTAATTAAGAACCAAGCAGATAAGAGAGAAATACTCTACGCGCAAAATCGTT 1560
Db 1501 CAAAGACTCCAGTTAATTAAGAACCAAGCAGATAAGAGAGAAATACTCTACGCGCAAAATCGTT 1560
Qy 1561 ACATACACCTTCAAAGCTAGAAACCAAGTGCCTGAAAGAAACTCCAATTAATAATACCAG 1620
Db 1561 ACATACACCTTCAAAGCTAGAAACCAAGTGCCTGAAAGAAACTCCAATTAATAATACCAG 1620
Qy 1621 TAAATTTCAACAGGAACAGACAAGTTAATGACAGGTTAATGACAGGTTCAATAGCCCTGAGAGCGGTGCC 1680
Db 1621 TAAATTTCAACAGGAACAGACAAGTTAATGACAGGTTAATGACAGGTTCAATAGCCCTGAGAGCGGTGCC 1680
Qy 1681 GCTCAGTGGAAATGGATCTCAACCAAGCACATATGGAGAGACTCCAAAAGAAAGGGAG 1740
Db 1681 GCTCAGTGGAAATGGATCTCAACCAAGCACATATGGAGAGACTCCAAAAGAAAGGGAG 1740
Qy 1741 CAAAAGTGTGGAGCCCTTGAAAGGGGTTGGATAAGGTTATCACTGTGCTCACCAGGA 1800
Db 1741 CAAAAGTGTGGAGCCCTTGAAAGGGGTTGGATAAGGTTATCACTGTGCTCACCAGGA 1800
Qy 1801 GCAAAAGGAGGGTCTGCGCAGAGAGCGGCCAGAGACTAAAGCTTCACTATAATGTGA 1860
Db 1801 GCAAAAGGAGGGTCTGCGCAGAGAGCGGCCAGAGACTAAAGCTTCACTATAATGTGA 1860
Qy 1861 CTAACTAGATTTAGTGAATCCAGATCAACTGTTGAATGAAATAATGTCTATCTTCCAA 1920
Db 1861 CTAACTAGATTTAGTGAATCCAGATCAACTGTTGAATGAAATAATGTCTATCTTCCAA 1920
Qy 1921 AGAAGCATGTTGACTTTGTGTAACAAAAGGGTTATACACTGAAAGTGTCAAAACACAGT 1980
Db 1921 AGAAGCATGTTGACTTTGTGTAACAAAAGGGTTATACACTGAAAGTGTCAAAACACAGT 1980
Qy 1981 TTGGGAAAGTGCACATGCAATTTGAAATTTAGAGTGTGCCAGCTTCAAAAACCGGATGG 2040
Db 1981 TTGGGAAAGTGCACATGCAATTTGAAATTTAGAGTGTGCCAGCTTCAAAAACCGGATGG 2040
Qy 2041 TGGGTATCAGGAGGCGGCTTAAAGGCGATGCTGGTGTACAAAAGATTTAGTGGAG 2100
Db 2041 TGGGTATCAGGAGGCGGCTTAAAGGCGATGCTGGTGTACAAAAGATTTAGTGGAG 2100
Qy 2101 ACATCTATCTAGCTGCAAGGTATAATTTGATGGAATTTCCATCTCTGCGGATGAGTGTG 2160
Db 2101 ACATCTATCTAGCTGCAAGGTATAATTTGATGGAATTTCCATCTCTGCGGATGAGTGTG 2160
Qy 2161 GGTGTGATACAGCTTACATAAAGACTGTATGATCGCTTTGATTTTAAAGTTCAATGGAA 2220
Db 2161 GGTGTGATACAGCTTACATAAAGACTGTATGATCGCTTTGATTTTAAAGTTCAATGGAA 2220
Qy 2221 CTACCAACTGTTTCTAAAGAGCTATCTTAAGACCAATATCTCTTTGTTTAAACAAA 2280
Db 2221 CTACCAACTGTTTCTAAAGAGCTATCTTAAGACCAATATCTCTTTGTTTAAACAAA 2280
Qy 2281 GATATTTATTTGTGATGAATCTAAATCAAGCCCATCTGTCTATTAATGTTACTGTCTTTT 2340
Db 2281 GATATTTATTTGTGATGAATCTAAATCAAGCCCATCTGTCTATTAATGTTACTGTCTTTT 2340
Qy 2341 TAAATCATGTTTGTGATATTAATTTGTTGACTTTCTTAGATTTCACTTCCATATGTG 2400
Db 2341 TAAATCATGTTTGTGATATTAATTTGTTGACTTTCTTAGATTTCACTTCCATATGTG 2400
Qy 2401 AATGTAAGCTCTTAACATGCTCTTTCTTAATGTTAATTTCTTCTGAAATTAACCAT 2460
Db 2401 AATGTAAGCTCTTAACATGCTCTTTCTTAATGTTAATTTCTTCTGAAATTAACCAT 2460


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Db 1261 ATAAAAATTAATGCGGGGATTAATAGACTATGATTTGGTGTGAAGATGATTTATCAACAG 1320
Qy 1321 GTGCTGTACTCCCGGAACATCACAGTTTACCAAGTACTGGACAGCAATCAAAATGGGGTGG 1380
Db 1321 GTGCTGTACTCCCGGAACATCACAGTTTACCAAGTACTGGACAGCAATCAAAATGGGGTGG 1380
Qy 1381 AATCTAAATCAATTAATCTCAGCCTTATGAGAAACACTGCGCAATAAATAAAGAAACAAAG 1440
Db 1381 AATCTAAATCAATTAATCTCAGCCTTATGAGAAACACTGCGCAATAAATAAAGAAACAAAG 1440
Qy 1441 AAAATGTATATCTCTTAAGTCTGCTGTAAGAAATGAAGAGTACTTTATGTTTCTCGAGC 1500
Db 1441 AAAATGTATATCTCTTAAGTCTGCTGTAAGAAATGAAGAGTACTTTATGTTTCTCGAGC 1500
Qy 1501 CAAAGACTCCAGTTAATAAGAACAGCAGCATAAGAGAGAAATCTCAATTAATAATCCAG 1560
Db 1501 CAAAGACTCCAGTTAATAAGAACAGCAGCATAAGAGAGAAATCTCAATTAATAATCCAG 1560
Qy 1561 ACATACACCTCAAAAGCTAGAAACAGTGCCTGAAAGAACTCAATTAATAATCCAG 1620
Db 1561 ACATACACCTCAAAAGCTAGAAACAGTGCCTGAAAGAACTCAATTAATAATCCAG 1620
Qy 1621 TAAATTTCAACAGGAACAGCAAGTAAATGACAGGTCTATTAGCCTGAGAGCGGTGCC 1680
Db 1621 TAAATTTCAACAGGAACAGCAAGTAAATGACAGGTCTATTAGCCTGAGAGCGGTGCC 1680
Qy 1681 GCTCAGTGAATTTGGATCTCAACCAAGCACATATGGAGAGACTCCAAAAAGAAAGGGAG 1740
Db 1681 GCTCAGTGAATTTGGATCTCAACCAAGCACATATGGAGAGACTCCAAAAAGAAAGGGAG 1740
Qy 1741 CCAAAGTGTGGAGCCTTGAAGGGGTGGATTAAGTTTCACTGTGCTCACCAGGA 1800
Db 1741 CCAAAGTGTGGAGCCTTGAAGGGGTGGATTAAGTTTCACTGTGCTCACCAGGA 1800
Qy 1801 GCAAAAGGAAGGGTCTGCGCAGAGACGGGCCAGAGACTTAAGCTTCACTATAATGTGA 1860
Db 1801 GCAAAAGGAAGGGTCTGCGCAGAGACGGGCCAGAGACTTAAGCTTCACTATAATGTGA 1860
Qy 1861 CTACAACTAGATTAGTGAATCCAGATCAACTGTGTAATGAATAATGTCTATTCTCCAA 1920
Db 1861 CTACAACTAGATTAGTGAATCCAGATCAACTGTGTAATGAATAATGTCTATTCTCCAA 1920
Qy 1921 AGAAGCATGTTGACTTTGTACAAAAGGGTTATACACTGAAGTGTCAACACAGTCAGATT 1980
Db 1921 AGAAGCATGTTGACTTTGTACAAAAGGGTTATACACTGAAGTGTCAACACAGTCAGATT 1980
Qy 1981 TTGGGAACTGACATGCAATTTGAAATTAAGTGAAGTGTGCCAGTTCAAAAACCGGATGG 2040
Db 1981 TTGGGAACTGACATGCAATTTGAAATTAAGTGAAGTGTGCCAGTTCAAAAACCGGATGG 2040
Qy 2041 TGGGTATCAGGAGGAGCGGCTTAAGGGCGATGCCCTGGGTTTACAAAAGATTAGTGGAG 2100
Db 2041 TGGGTATCAGGAGGAGCGGCTTAAGGGCGATGCCCTGGGTTTACAAAAGATTAGTGGAG 2100
Qy 2101 ACATCCTATCTAGCTCAAGGTATTAATTCAGATTCCTTCATCTCCGCGATGAGTGTG 2160
Db 2101 ACATCCTATCTAGCTCAAGGTATTAATTCAGATTCCTTCATCTCCGCGATGAGTGTG 2160
Qy 2161 GGTGTGATACAGGCTACATAAGACCTGTTATGATCGCTTTGATTTTAAAGTTCATTGGAA 2220
Db 2161 GGTGTGATACAGGCTACATAAGACCTGTTATGATCGCTTTGATTTTAAAGTTCATTGGAA 2220
Qy 2221 CTACCAACTGTGTTCTTAAAGAGCTATCTTAAGACCAATATCTCTTTGTTTTTAAACAAA 2280
Db 2221 CTACCAACTGTGTTCTTAAAGAGCTATCTTAAGACCAATATCTCTTTGTTTTTAAACAAA 2280
Qy 2281 GATATTTATTTGTGATGAATCTAAATCAAGCCCATCTGCTCATTAATGTTACTGTCTTTT 2340
Db 2281 GATATTTATTTGTGATGAATCTAAATCAAGCCCATCTGCTCATTAATGTTACTGTCTTTT 2340
Qy 2341 TAATCATGTGGTTTGTATATTAATTAATGTTGACCTTCTTAGATTCATCTCCATATGTG 2400
|||||
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Db 2341 TAATCATGTGGTTTGTATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2400
Qy 2401 AATGTAAGCTCTTAACATATGCTCTTTGTAATGTGTAATTTCTTTCTGAAATAAAACCAT 2460
Db 2401 AATGTAAGCTCTTAACATATGCTCTTTGTAATGTGTAATTTCTTTCTGAAATAAAACCAT 2460
Qy 2461 TTGTGAATAT 2470
Db 2461 TTGTGAATAT 2470

RESULT 12
ADR25674
ID ADR25674 standard; DNA; 2470 BP.
XX
AC ADR25674;
DT 21-OCT-2004 (first entry)
XX
DE Breast cancer prognosis marker #1535.
XX
KW ds; breast cancer; prognosis; gene expression; diagnosis.
XX
OS Homo sapiens.
XX
PN WO2004065545-A2.
XX
PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US001100.
XX
PR 15-JAN-2003; 2003US-00342887.
XX
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
XX
PI Van't Veer LJ, He Y;
XX
WPI; 2004-593473/57.
XX
Classifying a breast cancer patient according to prognosis comprises
determining the similarity between the level of expression of each of
five genes in a cell sample taken from patient, to control levels.
XX
Disclosure; SEQ ID NO 1535; 226pp; English.
XX
The invention relates to a method of classifying a breast cancer patient
according to prognosis by determining the similarity between the level of
expression of each of five genes for which markers are listed in the
specification, in a cell sample taken from the breast cancer patient, to
control levels of expression for each respective five genes to obtain a
patient similarity value. The methods are useful for classifying a breast
cancer patient according to prognosis. Kits and computer program products
are useful for data analysis using the diagnostic, prognostic and
statistical methods of the invention. This sequence corresponds to a
marker used in the method of the invention.
XX
Sequence 2470 BP; 767 A; 488 C; 536 G; 679 T; 0 U; 0 Other;

Query Match 100.0%; Score 2470; DB 13; Length 2470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGCGGGCGGAAGCGGCCACAAACCGCGCGATCGAAAGATTCTTAGGAACGCCGTACCA 60
Db 1 TTGGCGGGCGGAAGCGGCCACAAACCGCGCGATCGAAAGATTCTTAGGAACGCCGTACCA 60
Qy 61 GCCGCGTCTCTCAGGACAGCAGGCCCTGTCTCTTCTGTGCGGCGCGCTCAGCGCGTGC 120
Db 61 GCCGCGTCTCTCAGGACAGCAGGCCCTGTCTCTTCTGTGCGGCGCGCTCAGCGCGTGC 120
Qy 121 TCCGCGCCCTCAGGTTCTTTTCTTAATTCCTCAATAAATTCCTGCAAGAGGACTATGAAGATT 180
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QY 2341 TAATCATGTGTTTGTATATTAATAATTTGATCTTTCAGTTCACCTTCCATATGTG 2400
 Db |||||||
 2341 TAATCATGTGTTTGTATATTAATAATTTGATCTTTCAGTTCACCTTCCATATGTG 2400
 QY 2401 AATGTAAGCTCTTAACATATGTCCTTTGTAATGTAATTTCTTTGGAATAAAACCAT 2460
 Db |||||||
 2401 AATGTAAGCTCTTAACATATGTCCTTTGTAATGTAATTTCTTTGGAATAAAACCAT 2460
 QY 2461 TTGTGAATAT 2470
 Db |||||||
 2461 TTGTGAATAT 2470

RESULT 13
 ADU05979
 ID ADU05979 standard; DNA; 2470 BP.
 AC ADU05979;
 XX
 DT 27-JAN-2005 (first entry)
 XX Novel bronchial cancer-associated human gene SegID201.
 DE
 XX
 XX bronchial cancer; cytostatic; tumour-associated protein;
 KW cancer detection; metastasis; tumour; gene; ds; human.
 KW
 XX Homo sapiens.
 OS
 XX DE10316701-A1.
 PN
 XX 04-NOV-2004.
 PD
 XX
 XX 09-APR-2003; 2003DB-01016701.
 PF
 XX
 XX 09-APR-2003; 2003DB-01016701.
 PR
 XX (HINZ/) HINZMANN B.
 PA (HERM/) HERMANN K.
 PA (CAST/) HEIDEN CASTANOS-VELEZ E.
 XX
 PI Mennerich D, Bruemendorf T, Heiden E, Hermann K, Kinnemann H;
 PI Li X, Roepcke S, Staub E, Hinzmann B, Rosenthal A, Pilarsky C;
 XX
 DR WPI; 2004-786403/78.
 DR P-PSDB; ADU06466.
 XX
 PT New nucleic acid, and derived proteins, useful for diagnosis of bronchial
 PT cancer and in screening for therapeutic and diagnostic agents.
 XX
 PS Claim 1; SEQ ID NO 201; 1381pp; German.
 XX
 CC This invention relates to a novel isolated nucleic acid associated with
 CC bronchial cancer comprising 489 defined sequences given in the
 CC specification. The invention may be useful for the production of
 CC compounds with a cytostatic activity through the inhibition of expression
 CC or activity of tumour-associated proteins. The novel DNA sequences and
 CC the proteins/peptides encoded by them are used for detecting bronchial
 CC cancer or determining the risk of developing it and to screen for
 CC specific binding partners of the DNA or protein sequences, where the
 CC binding partners are potentially useful as agents for treating or
 CC diagnosing bronchial cancer. The DNA or protein sequences can also be
 CC used for prognosis, detection of metastases and for secondary treatment
 CC (of tumours that have been stabilised or are no longer detectable).
 CC Detecting abnormal expression of the DNA sequences provides early
 CC diagnosis of bronchial cancers. The present sequence is that of a novel
 CC bronchial cancer-associated human gene sequence of the invention.
 XX
 SQ Sequence 2470 BP; 767 A; 488 C; 536 G; 679 T; 0 U; 0 Other;

Query Match
 Best Local Similarity 100.0%; Score 2470; DB 13; Length 2470;
 Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCGGGCGGAAGCGGCCCAACCGCGCATCGAAAGATTCTTAGGAACGCGGTACCA 60
 Db |||||||
 1 TTGGCGGGCGGAAGCGGCCCAACCGCGCATCGAAAGATTCTTAGGAACGCGGTACCA 60
 QY 61 GCGCGCTCTCTCAGGACAGCAGCGCCCTCTCTTCTGTCGGGCGCGCTCAGCGGTGCC 120
 Db |||||||
 61 GCGCGCTCTCTCAGGACAGCAGCGCCCTCTCTTCTGTCGGGCGCGCTCAGCGGTGCC 120
 QY 121 TCGCGCCCTCAGGTCTCTTTTCTTAATTCAAATAAATCTTCAAGAGGACTATGAAGAAT 180
 Db |||||||
 121 TCGCGCCCTCAGGTCTCTTTTCTTAATTCAAATAAATCTTCAAGAGGACTATGAAGAAT 180
 QY 181 ATGATGAACCTTCTCAAAATATTATGAATTAACATGAATTTGGGACAGGTGGCTTGC 240
 Db |||||||
 181 ATGATGAACCTTCTCAAAATATTATGAATTAACATGAATTTGGGACAGGTGGCTTGC 240
 QY 241 AGGTCAAACTTCGCTGCCATATCTTACCTGGAGAGATGTAGCTATAAAATCATGGATA 300
 Db |||||||
 241 AGGTCAAACTTCGCTGCCATATCTTACCTGGAGAGATGTAGCTATAAAATCATGGATA 300
 QY 301 AAAACACACTAGGAGGTGATTTGCCCGGATCAAAACCGAGATTGAGGCTTTGAAGAACC 360
 Db |||||||
 301 AAAACACACTAGGAGGTGATTTGCCCGGATCAAAACCGAGATTGAGGCTTTGAAGAACC 360
 QY 361 TGAGACATCAGCATATATGTCAACTCTACCTACCTAGCTAGAGACAGCAACAAATATTC 420
 Db |||||||
 361 TGAGACATCAGCATATATGTCAACTCTACCTACCTAGCTAGAGACAGCAACAAATATTC 420
 QY 421 TGGTCTTGTAGTACTGCTGAGGAGAGCTGTTTGAATTAATTTCCAGGATCGCC 480
 Db |||||||
 421 TGGTCTTGTAGTACTGCTGAGGAGAGCTGTTTGAATTAATTTCCAGGATCGCC 480
 QY 481 TGTCAAGAGAGGAGACCGGGTGTCTTCGGTCAGATAGTATCTGCTGTGTATGTGC 540
 Db |||||||
 481 TGTCAAGAGAGGAGACCGGGTGTCTTCGGTCAGATAGTATCTGCTGTGTATGTGC 540
 QY 541 ACAGCAGGGCTATGCTCAAGGAGACCTCAAGCCAGAAAATTTGCTGTTGATGAATATC 600
 Db |||||||
 541 ACAGCAGGGCTATGCTCAAGGAGACCTCAAGCCAGAAAATTTGCTGTTGATGAATATC 600
 QY 601 ATAAATTAAGCTGATGACCTTTGCTCTGTCGCAAAACCCCAAGGGTAAACAGGATACC 660
 Db |||||||
 601 ATAAATTAAGCTGATGACCTTTGCTCTGTCGCAAAACCCCAAGGGTAAACAGGATACC 660
 QY 661 ATCTACAGACATGCTGTGGAGTCTGGCTTATGTCAGCACCTGAGTTAATACAGGCAAT 720
 Db |||||||
 661 ATCTACAGACATGCTGTGGAGTCTGGCTTATGTCAGCACCTGAGTTAATACAGGCAAT 720
 QY 721 CATATCTTGGATCAGAGGAGATGTTGGAGCATGCGGATCTGTTATATGTTCTTATGT 780
 Db |||||||
 721 CATATCTTGGATCAGAGGAGATGTTGGAGCATGCGGATCTGTTATATGTTCTTATGT 780
 QY 781 GTGGATTTCTACCATTTTCATGATGATGATGATGATGATGATGATGATGATGATG 840
 Db |||||||
 781 GTGGATTTCTACCATTTTCATGATGATGATGATGATGATGATGATGATGATGATG 840
 QY 841 GAAATATATGATGTTCCCAAGTGGCTCTCTCCAGTAGCATCTGCTTCTTCAACAAATGC 900
 Db |||||||
 841 GAAATATATGATGTTCCCAAGTGGCTCTCTCCAGTAGCATCTGCTTCTTCAACAAATGC 900
 QY 901 TGCAGGTGGACCAAGAAACCGATTTCTATGAATAATCTATGAACCATCTCCGTGATCA 960
 Db |||||||
 901 TGCAGGTGGACCAAGAAACCGATTTCTATGAATAATCTATGAACCATCTCCGTGATCA 960
 QY 961 TGCAGATTTACAATCTATCTCTGTTAGTGCAGCAAGCAATCTTTTATTCACCTCGATG 1020
 Db |||||||
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 QY 1021 ATGATTGGGTAAACGAACCTTTCTGTACATCAAGAAAACACAGGCAACAAATGAGGAT 1080
 Db |||||||
 1021 ATGATTGGGTAAACGAACCTTTCTGTACATCAAGAAAACACAGGCAACAAATGAGGAT 1080
 QY 1081 TAATTTCACTGTGGCAGTATGATCACTACGGCTACCTATCTTCTTCTAGCAAGA 1140

Db 1081 |||||TAATTTCACTGTGGAGTAGATCACTCAGCGCTACCTATCTTCTGCTTAGCCAGA 1140
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Db 1141 AGGCTCGGGGAAACCAAGTTCGTTTAAAGGCTTCTTCTTCTCTGTCGACAGCCAGTG 1200
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Db 1261 ATAAAAATATATGTGGGGGATTAATAGACTATGATTTGGTGTGAAGATGATTTATCAACAG 1320
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Db 1441 AAAATGTATATACTCTCTAAGTCTGCTGTAAAGAAATGAAGAGTACTTTATGTTTCTTGAGC 1500
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Db 1681 GCTCAGTGGAAATGGATCTCAACAGCACAATATGAGAGAGACTCCAAAAGAAAGGGAG 1740
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Db 1861 CTACAACATAGTAGTGAATCCAGATCAACTGTTGAATGAATGAATGCTTATCTTCCAA 1920
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Db 1921 AGAAGCATGTTGATTTGTACAAAAGGTTATACACTGAAGTGTCAAAACAGTCAAGATT 1980
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Db 1981 TTGGGAAAGTGACAATGCAATTTGAAATTAGAGTGTGCCAGCTTCAAAAACCCGATGTGG 2040
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Db 2041 TGGGTATCAGAGGACGGCTTAAGGCCATGCTGGGTTTACAAAAGATTAGTGGAG 2100
Qy 2101 ACATCTATCTAGTCGAAGTATAATTGATGATTTCTTCCATCTCGCGGATGAGTGTG 2160
Db 2101 ACATCTATCTAGTCGAAGTATAATTGATGATTTCTTCCATCTCGCGGATGAGTGTG 2160
Qy 2161 GGTGTGATACAGCCTACATAAAGACTGTGTTATGATCGCTTTGATTTAAAGTTCAATTGGAA 2220

Db 2161 GGTGTGATACAGCCTACATAAAGACTGTGTTATGATCGCTTTGATTTAAAGTTCAATTGGAA 2220
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Db 2221 CTACCAACTGTTTCTAAAGAGCTATCTTAAGACCAATATCTCTTTGTTTTAAACAAA 2280
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Qy 2401 AATGTAAGCTCTTAACATATGCTCTTTGTAATGTCTAAATTTCTTCTGAAATAAACCAT 2460
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Qy 2461 TTGTGAATAT 2470
Db 2461 TTGTGAATAT 2470

RESULT 14
ADX07296
ID ADX07296 standard; DNA; 2470 BP.
XX ADX07296;
AC ADX07296;
XX 21-APR-2005 (first entry)
DT
XX Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1861.
DE
XX cytostatic; cyclin-dependent kinase; cdk; biomarker; gene; ds.
XX
XX Homo sapiens.
OS
XX
XX PN WO2005012875-A2.
XX
XX PD 10-FEB-2005.
XX
XX PF 29-JUL-2004; 2004WO-US024424.
XX
XX PR 29-JUL-2003; 2003US-0490890P.
XX
XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX
XX DR WPI; 2005-163068/17.
XX
XX DR P-PSDB; ADX07297.
XX
XX PT Biomarkers useful for predicting or determining the response of a mammal
XX
XX PT to a cancer treatment comprising administration of a modulator of cyclin-
XX
XX PT dependent kinase activity.
XX
XX PS Claim 5; SEQ ID NO 1861; 141pp; English.
XX
XX CC This invention describes a novel method of predicting or determining
XX
XX CC whether a mammal will respond or is responding to an anti-cancer agent
XX
XX CC that modulates cyclin-dependent kinase (cdk) activity. The method
XX
XX CC comprises measuring the level of one or more biomarkers selected from
XX
XX CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
XX
XX CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the
XX
XX CC invention is utilized in a kit for determining or predicting whether
XX
XX CC patient would be susceptible or resistant to treatment by an agent
XX
XX CC modulating cdk activity. The invention also describes a method for
XX
XX CC utilizing individualized genetic profiles for treating diseases and
XX
XX CC disorders based on patient's response and molecular level, specialized
XX
XX CC microarrays comprising the biomarkers described, antibodies directed
XX
XX CC against the biomarkers and a cell culture model to identify biomarkers.
XX
XX CC The cdk modulator is preferably N-5-[[5-(1,1-Dimethylethyl)-2-oxazoly

CC tartaric acid salt. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published/pct sequences. This
CC sequence encodes a biomarker used in the method of the invention.

XX
SQ Sequence 2470 BP; 767 A; 488 C; 536 G; 679 T; 0 U; 0 Other;

Query Match 100.0%; Score 2470; DB 14; Length 2470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TTGGCGGGGGAAGCGGCCACACCGCGGATCGAAAGATTCTTAGGAACGCGTACCA 60
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DB 61 GCGCGCTCTCTCAGGACAGCAGCGCCCTGTCTTCTGTGGGCGCGCTCAGCGCGTGC 120
QY 121 TCGGCCCTCAGGTTCTTTTCTAATTCMAATAAACTTGCAAGAGACTATGAAGAATT 180
DB 121 TCGGCCCTCAGGTTCTTTTCTAATTCMAATAAACTTGCAAGAGACTATGAAGAATT 180
QY 181 ATGATCAACTTCTCAAAATATTATGAATATCATGAACATATGGGACAGTGGCTTGCAA 240
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DB 421 TGGTCTTGAGTACTGCTCGGAGGAGAGTGTTCGACTATATAATTTCCAGGATCGCC 480
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DB 481 TGTCAAGAGAGAGACCGGGTGTCTTCGGTCAGATAGTATCTGCTGTGCTTATGTGC 540
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DB 841 GAAAAATATGATGTTCCCAAGTGGCTCTCTCCAGTAGCATTTCTGCTTCTTCAACAAATGC 900
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DB 1141 AGGCTGGGGAAAAACAGTTCGTTTAAAGGCTTTCTTTCTCTGTGGAAAGCCAGTG 1200
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DB 1261 ATAAAAAATATCTGGCGGATTAATAGACTATGATTTGGTGTGAAGATATTTTATCAACAG 1320
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DB 1321 GTGCTGCTACTCCCGAACATCACAGTTTACCAAGTACTTGGACAGAAATCAAAATGGGGTGG 1380
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DB 1381 AATCTAAATCATTAATCCAGCCTTATGACAGAAACCTTGCAGAAATAAATTAAGAAACAAAG 1440
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DB 1441 AAAATGTATATACTCCTTAAGTCTGTAAACAAATGAAGAGTACTTATGTTTCTCTGAGC 1500
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DB 1681 GCTCAGTGGAAATTTGGATCTCAACCAAGCACATATGAGAGAGAGACTCCAAAAGAAAGGGAG 1740
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DB GGTGTATACAGCTACATAAAGACTGTTATGATCGCTTTGATTTAAAGTTTCATTGGAA 2220
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DB TTGTGAATAT 2470

RESULT 15
ADW93565
ID ADW93565 standard; cDNA; 2470 BP.

XX AC ADW93565;
XX DT 05-MAY-2005 (first entry)
XX Human maternal embryonic leucine zipper kinase, MELK, cDNA #1.
DE Maternal embryonic leucine zipper kinase; ss; gene; drug screening;
XX angiogenesis disorder; antiangiogenic; cardiovascular disease; apoptosis;
KW cancer; cytostatic; neoplasm; diagnosis; gene therapy.
XX OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 171..2126
FT /*tag= a
FT /product= "MELK"
PN WO2005016279-A2.
XX PD 24-FEB-2005.
XX 12-AUG-2004; 2004WO-US026231.
XX PR 14-AUG-2003; 2003US-0495193P.
XX (EXEL-) EXELIXIS INC.
PI Kadyk L, Francis GR, Heuer TS, Lickteig K;
XX WPI: 2005-173218/18.
DR P-PSDB; ADW93570.
XX Identifying candidate RAC pathway modulating agents useful for diagnosing
PT or treating e.g. cancer, comprises screening for agents that modulate the
PT activity of Maternal Embryonic Leucine Zipper Kinase (MELK).

XX Disclosure; SEQ ID NO 1; 52pp; English.

CC The invention relates to identifying a candidate RAC pathway modulating agent comprising screening for agents that modulate the activity of Maternal Embryonic Leucine Zipper Kinase (MELK). Also included are modulating a RAC pathway of a cell or in a mammalian cell and diagnosing a disease in a patient. In identifying a candidate RAC pathway-modulating agent, the assay system comprises cultured cells that express the MELK polypeptide. The cultured cells additionally have defective RAC function. The methods are useful for diagnosing or treating cancer or for identifying modulators of RAC pathway, which may be utilized as therapeutic targets for disorders associated with defective RAC function, such as cancer, angiogenic disorder and apoptotic disorders. The present sequence is a human cDNA encoding MELK.

XX Sequence 2470 BP; 767 A; 488 C; 536 G; 679 T; 0 U; 0 Other;

Query Match 100.0%; Score 2470; DB 14; Length 2470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TTGGCGGGCGGAAGCGGCCCAACCCGGCGATCGAAAGATTCTTAGNACCCCGTACCA 60
QY 61 GCCGCTCTCTCAGGACAGCGGCCCTCTCTCTCTGTCGGCGCGCTCAGCCGTCGCC 120
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QY 121 TCCGCCCTCTCAGGTTCTTTTCTAATTCCAAATAAACTTGCAGAGGACTATGAAGATT 180
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QY 181 ATGATGAATCTCTCAAAATATATGAATTAATGAATTAATGAATTAATGAATTAATGA 240
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DB 241 AGGTCAAACTTGCCTGCCATATCTTCTACTGGAGAGATGTTAGTATATAAAATCATG 300
QY 301 AAAACACACTAGGAGTGAATTTGCCCGGATCAAAAACCGGATCGGCTTTGAAGAAC 360
DB 301 AAAACACACTAGGAGTGAATTTGCCCGGATCAAAAACCGGATCGGCTTTGAAGAAC 360
QY 361 TGAGACATCAGCATATATGTCACTCTACCATGTCTAGACAGACCCACAAATATTTCA 420
DB 361 TGAGACATCAGCATATATGTCACTCTACCATGTCTAGACAGACCCACAAATATTTCA 420
QY 421 TGGTTCTTTGAGTACTGCCCTGGAGGAGAGCTGTTTGAATATATTTCCAGGATCGCC 480
DB 421 TGGTTCTTTGAGTACTGCCCTGGAGGAGAGCTGTTTGAATATATTTCCAGGATCGCC 480
QY 481 TGTCTAGAGAGGAGACCCCGGGTTGTCTTCGGTCAGATAGTATCTGCTGTTTATGTGC 540
DB 481 TGTCTAGAGAGGAGACCCCGGGTTGTCTTCGGTCAGATAGTATCTGCTGTTTATGTGC 540
QY 541 ACAGCCAGGGCTATGCTCAAGGACCTCAAGCAGAAAATTTGCTGTTTATGATATTC 600
DB 541 ACAGCCAGGGCTATGCTCAAGGACCTCAAGCAGAAAATTTGCTGTTTATGATATTC 600
QY 601 ATAAATTAAGCTGATTGACTTTTGTCTGTGCAAAACCCAGGGTAAACAGGATTACC 660
DB 601 ATAAATTAAGCTGATTGACTTTTGTCTGTGCAAAACCCAGGGTAAACAGGATTACC 660
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DB 661 ATCTACAGACATGCTGTGGAGTCTGGCTTATGTCAGCACCTGAGTTAAATACAAGGCA 720
QY 721 CATATCTTGGATCAGAGGAGATGTTGGAGATGCGGATCTGTTATATGTTCTTATGT 780
DB 721 CATATCTTGGATCAGAGGAGATGTTGGAGATGCGGATCTGTTATATGTTCTTATGT 780

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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2470	100.0	2470	4	US-09-870-937-9 Sequence 9, Appli
3	214	8.7	245	3	US-09-513-999C-11495 Sequence 11495, A
4	206.8	8.4	1863	3	US-09-949-016-4303 Sequence 4303, Ap
5	197.6	8.0	2224	3	US-09-949-016-2384 Sequence 2384, Ap
6	197.6	8.0	2224	3	US-09-949-016-2385 Sequence 2385, Ap
7	197.6	8.0	2950	3	US-09-949-016-1546 Sequence 1546, Ap
8	197.6	8.0	2950	3	US-09-949-016-1547 Sequence 1547, Ap
9	196	7.9	2175	3	US-09-984-890-1 Sequence 1, Appli
10	196	7.9	2175	3	US-10-274-194-1 Sequence 1, Appli
11	196	7.9	2175	3	US-10-760-407-1 Sequence 1, Appli
12	188.8	7.6	1647	3	US-09-101-146-44 Sequence 44, Appl
13	188.6	7.6	1736	3	US-08-557-006C-37 Sequence 37, Appl
14	188.6	7.6	1783	3	US-08-557-006C-36 Sequence 36, Appl
15	181.2	7.3	2210	3	US-09-949-016-1699 Sequence 1699, Ap
16	173.8	7.0	2698	2	US-08-677-298-1 Sequence 1, Appli
17	173.8	7.0	2912	3	US-09-949-016-2363 Sequence 2363, Ap
18	172.6	7.0	1742	3	US-08-557-006C-38 Sequence 38, Appl
19	172.6	7.0	2652	3	US-08-557-006C-39 Sequence 39, Appl
20	172.6	7.0	2761	3	US-08-557-006C-24 Sequence 24, Appl
21	170.6	6.9	2914	3	US-09-949-016-343 Sequence 343, Ap
22	170.4	6.9	3609	3	US-09-799-875-6 Sequence 6, Appli
23	170.4	6.9	5983	3	US-09-799-875-4 Sequence 4, Appli

24	167.8	6.8	1539	3	US-09-633-328B-1 Sequence 1, Appli
25	159.4	6.5	3857	3	US-10-464-939-1 Sequence 1, Appli
26	156	6.3	1929	3	US-09-359-161-4 Sequence 4, Appli
27	155.4	6.3	4790	3	US-10-464-939-3 Sequence 3, Appli
28	149.8	6.1	1590	3	US-09-554-726A-4 Sequence 4, Appli
29	149.8	6.1	2257	3	US-09-554-726A-6 Sequence 6, Appli
30	149.6	6.1	2738	3	US-09-554-726A-9 Sequence 9, Appli
31	149.2	6.0	1254	3	US-09-248-796A-4338 Sequence 4338, Ap
32	149.2	6.0	1747	3	US-08-557-006C-44 Sequence 44, Appl
33	148	6.0	1787	3	US-09-554-726A-13 Sequence 13, Appl
34	147	6.0	2334	3	US-10-003-690-3 Sequence 3, Appli
35	147	6.0	2337	3	US-10-116-326-1 Sequence 1, Appli
36	147	6.0	2337	3	US-10-803-277-1 Sequence 1, Appli
37	147	6.0	2980	3	US-10-003-690-1 Sequence 1, Appli
38	145	5.9	1902	3	US-09-487-558B-337 Sequence 337, App
39	143.2	5.8	2899	3	US-09-774-528-112 Sequence 112, App
40	143.2	5.8	2899	3	US-10-120-988-112 Sequence 112, App
41	139.8	5.7	2112	3	US-10-116-326-5 Sequence 5, Appli
42	139.8	5.7	2112	3	US-10-803-277-5 Sequence 5, Appli
43	137.6	5.6	2902	3	US-09-579-664B-4 Sequence 4, Appli
44	137.6	5.6	2902	3	US-10-355-975A-4 Sequence 4, Appli
45	137.6	5.6	2902	5	US-09-980-464-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-880-107-1725
; Sequence 1725, Application US/09880107
; Patent No. 6974667
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1725
; LENGTH: 2470
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. 6974667 D79997
US-09-880-107-1725

Query Match 100.0%; Score 2470; DB 4; Length 2470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-870-937-9
; Sequence 9, Application US/09870937
; Patent No. 6974867
; GENERAL INFORMATION:
; APPLICANT: Wu, Bin
; APPLICANT: Seeley, Todd
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEOPLASTIC DISEASE USING
; TITLE OF INVENTION: CHEMOTHERAPY AND RADIATION SENSITIZERS
; FILE REFERENCE: 200130.514/PP-01623.002
; CURRENT APPLICATION NUMBER: US/09/870,937
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2470
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-870-937-9

Query Match 100.0%; Score 2470; DB 4; Length 2470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-513-999C-11495
; Sequence 11495, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
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; SEQ ID NO 11495
; LENGTH: 245
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-11495

Query Match      8.7%; Score 214; DB 3; Length 245;
Best Local Similarity 95.7%; Pred. No. 1.4e-48;
Matches 220; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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RESULT 4
US-09-949-016-4303
; Sequence 4303, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4303
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4303

Query Match      8.4%; Score 206.8; DB 3; Length 1863;
Best Local Similarity 55.4%; Pred. No. 3.6e-46;
Matches 469; Conservative 0; Mismatches 362; Indels 15; Gaps 3;
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Qy 212 TGAAACTATTGGGACAGGTGGCTTTGCAAGGTCAAACTTGCCTGCCATATCTTACTCG 271
Db 86 TGACACGCTGGGGGTGGCGACCTTGGCAAGTGAAGTTGGCAACATGATTCAGCTGG 145
Qy 272 AGAGATGGTGTATATAAAATCATGATAAAACACACTAGGGAG-----TGATTTGCC 325
Db 146 GCATAAAGTAGCTGTGAAGATACTCAATCGACAGAAGATTTCGGAGCCTTGAATGTGTTAGG 205
Qy 326 CCGGATCAAAACGGAGATTGAGCCCTTGAAGAACCTTGAGACATCAGCATATATGTCACCT 385
Db 206 AAAAAATCCGACAGAAAATTCAGAACTCAAGCTTTTCAGGCAATCTCTATATAATTAACCT 265
Qy 386 CTACCATGTGTAGAGACAGCAACAAAATATTCATGGTTCTTGTAGTACTGCCCTGGAGG 445
Db 266 GTACACAGTTCATCAGTACACCATCTGATATTTTCATGGTGTGATGATATGTCTCAGAGG 325
Qy 446 AGAGCTGTTTGTACTATATAAATTTCCAGGATCGCTGTGAGAGAGGAGACCGGGTTGT 505
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Db 326 AGAGCTATTGATATATCTGTAAGAAATGAAGGCTGGATGAAAGAAAGTGGCGTCT 385
Qy 506 CTTCCGTCAGATAGTATCTGCTGTGTTATGTGTCACAGCCAGGCTATGCTCACAGGGA 565
Db 386 GTTCCAAACAGATCTTCTCGTGTGGATTAATGTGTCAGGCGATATGGTGTGTCATAGGA 445
Qy 566 CTTCAAGCCAGAAATTTGCTGTGTTGATGATATCAATAATTAAGTGTGATGCTTTGG 625
Db 446 TTTGAAACCTGAAATGTCTGCTGTGATGACACATGAATGCAAGATAGCTGATTTGG 505
Qy 626 TCTCTGTGCAAAACCCAGGTAACAGGATTAACCATCTACACACATGCTGTGCGAGTCT 685
Db 506 TCTTTC-----AAACATGATGTCAGATGTGTAATTTTAAAGAAAGTTGTGGCTACC 559
Qy 686 GGCTTATGACGACCTGAGTTAATAACAAGCAATCATATCTTTGGATCAGAGGCAGATGT 745
Db 560 CAACTATGCTGCACCAAGAGTAATTTTCAGGAGATTTGATGCAAGGCCAGAGGTAGATAT 619
Qy 746 TTGGAGCATGGGCATAGTGTATATGTTCTTATGTGTGATTTCTACCAATTTGATGATGA 805
Db 620 ATGGACAGTGGGTTATTCTCTATGCTTTATTTATGTTGGAACCTTTCCATTTGATGATGA 679
Qy 806 TAATGTAATGGCTTTATACAGAGGATTAAGAGGAAATATGATGTTCCCAAGTGGCT 865
Db 680 CCAATGCGCACTCTTTTAAAGAGATATGTGATGGATCTTCTATCCCTCAATATTT 739
Qy 866 CTCCTCCAGTAGCATTTCTGCTTCTCAACAAATGCTGCAGGTGGAACCCAAAGAAACGGAT 925
Db 740 AATCTCTCTGTGATAGCTTTTGAACAATGCTGCAGGTGATCCCATGAAGAGGC 799
Qy 926 TTTATGAAAAATCTATTGAACCATCCCTGGATCATGCAAGA---TTACAATATCTGT 982
Db 800 CACAATCAAGATATCAGGGAACATGAATGGTTTAAACAGGACCTTTCCAAATATCTCT 859
Qy 983 TGAGTGGCAAGCAAGAACCTTTTATTCACCTCGATGATGTTGGTGAACAGAACTTTC 1042
Db 860 TCTGAGGATCCATCATATAGTTCAACCATGATGATGATGAAGCCCTTAAAGAAAGTATG 919
Qy 1043 TGTACA 1048
Db 920 TGAAGA 925

RESULT 5
US-09-949-016-2384
; Sequence 2384, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2384
; LENGTH: 2224
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2384

Query Match 8.0%; Score 197.6; DB 3; Length 2224;
Best Local Similarity 52.4%; Pred. No. 1.3e-43;
Matches 487; Conservative 0; Mismatches 434; Indels 9; Gaps 2;

Qy 214 AAACATTTGGGACAGGTGGCTTTGCAAGGTCAAAGTTCGCTGCCATATCTTACTTGGAG 273
Db 71 AGACCAATTGGCAAGGGTAATTTTGGCAAGGTGAAGTTGGCCGACACATCTGACTGGGA 130
Qy 274 AGATGCTAGCTATATAAAATCATGGATATAAAACACACTAGGAGTGAATTTGCCCGCATCA 333
Db 131 AAGAGGTAGCTGTGAAGATCATTTGACAGACTCAACTGAATCTCTCCAGCCTCCAGAAAC 190
Qy 334 AAACG---GAGATTGAGGCTTTGAAGAACCTGAGACATCAGCATATATGTCACCTTACC 390
Db 191 TATTCGCGAAGTAAGAAATAATGAAGTTTGAATCATCCCAACATAGTAAATATTTTG 250
Qy 391 ATGTGCTAGACAGCAGCAACAAATATTCATGGTCTTGGAGTACTGCCCTGGAGGAGAGC 450
Db 251 AAGTATTGAGACTGAGAAACCGCTTACCTTTGTCAATGGAGTACGCTAGTGGCGGAGAGG 310
Qy 451 TGTGTTGACTATATAATTTCCAGAGTGGCTGTGCAAGAGGAGAGCCCGGTTGTCTTCC 510
Db 311 TATTTGATTACCTAGTGGCTCATGGCAGGATGAAGAAAGAGGCTCGAGCCAAATTTCC 370
Qy 511 GTCAGATAGTATCTGCTGTGTTATGTGCAAGCCAGGCTATGCTCACAGGACCTCA 570
Db 371 GCCAGATAGTGTCTGCTGTGAGTACTGTCAACAGAAAGTTTATTTGTCATAGAGACTTAA 430
Qy 571 AGCCAGAAAATTTGCTGTGTTGATGATATCATATAAATTAAGCTGATTTGACTTTGCTCT 630
Db 431 AGGCGAAGAAACCTGCTTGGATGCTGATATGAACATCAAGATTGACAGCTTTGGCTTCA 490
Qy 631 GTGCAAAACCCAGGTAACAGGATTAACATCTACAGACATGCTGTGGAGTCTGGCTT 690
Db 491 GCAATGAATTC-----ACCTTTGGGAACAAGCTGGACACCTTCTGTGGAGTCCCCCTT 544
Qy 691 ATGACGACCTCAGTTAATAACAGGCAATCATATCTTTGGATCAGAGGAGAGTGTGGA 750
Db 545 ATGCTGCCCAAGAACTTTCCAGGCAAAATAATGATGACCCCGAGGTGGATGTGGA 604
Qy 751 GCATGGGCATCTGTTATATGTTCTTATGTGGAATTTTACCATTTGATGATGATG 810
Db 605 GCCTAGGAGTTATCTCTCTATACACTGCTGAGCGGATCCCTTGTGATGACAGAAC 664
Qy 811 TAATGGCTTTATACAAAGAGATTATGAGAGGAAATATGATGTTCCCAAGTGGCTCTCTC 870
Db 665 TCAGAGAGCTGGGGAACGGTACTGAGGGGAAATACCGTATTCATCTACATGTCCA 724
Qy 871 CCAGTAGCATTTCTGCTTCTTCAACAAATGCTGAGGTGGAACCCAAAGAAACCGATTTCTA 930
Db 725 CGGACTGTGAAACCTGCTTAAAGAAATTTCTCATTTCTTAATCCAGCAAGAGAGCACCTT 784
Qy 931 TGAATAATCTATTGAACCATCCCTGGATCATGCAAGATTACAACTATCTCTGTTAGTGGC 990
Db 785 TAGAGCAATCATGAAAGATCGATGGTGAATGTGGGTCAAGAGATGATGAACTAAAGC 844
Qy 991 AAAGCAAGAACTCTTTTATTCACCTCGATGATGTTGCTTAACAGAACTTTCTGTACATC 1050
Db 845 CTTAGCTGGAGCACTCCCTGACTACAAGAGCCCGGGGACAGAGCTGATGGTGTCCA 904
Qy 1051 ACAGAAACAAAGGCAAAACAAATGAGGATTTAAATTTCACTGTGGCAGTATGATCACTCA 1110
Db 905 TGGGTTATACAGGGAAGAGATCCAGGACTCGCTGTGGGCCAGAGATACACAGAGGTGA 964
Qy 1111 CGGCTACCTATCTTCTGCTTTCTAGCCAAGA 1140
Db 965 TGGCCACCTATCTGCTCTCTGGGCTACAAGA 994

RESULT 6
US-09-949-016-2385
; Sequence 2385, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2384
; LENGTH: 2224
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2384

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FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2385
LENGTH: 2224
TYPE: DNA
ORGANISM: Human
US-09-949-016-2385

Query Match      8.0%; Score 197.6; DB 3; Length 2224;
Best Local Similarity 52.4%; Pred. No. 1.3e-43;
Matches 487; Conservative 0; Mismatches 434; Indels 9; Gaps 2;

QY 214 AAACATTTGGGACAGGTGGCTTTGCAAGGTCAAACTTGCCTGCCATATCCTTACTGGAG 273
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
71 AGACCATTTGGCAAGGTAATTTTGGCAAGGTGAAGTTGGCCCGACACATCCTGACTGGGA 130
QY 274 AGATGGTAGCTATAAAAAATCATGCATATAAAACACACTAGGGAGTGATTTGCCCGGATCA 333
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
131 AAGAGTAGTGTGAAGATCATTTGACAGACTCACTGAATCTCTCCAGCTCCAGAAC 190
QY 334 AAACG---GAGATTGAGGCCCTTGAAGAACTTGACATCAGCATATATGTCAACTTACC 390
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
191 TATTCGCGAAGTAAGAATAATGAAGTTTGAATCATCCACATAGTAAATATTATTTG 250
QY 391 ATGTGTAGACAGCCACAAATATTCACTGTTCTTGAGTACTGCCCTGGAGGAGC 450
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
251 AAGTGATTGAGCTGAGAAACCTCTACCTTGTCTATGAGTAGCTAGTGGCGGAGAGG 310
QY 451 TGTTTCACTATATAATTTCCAGGATGCGCTGTGCAAGAGGAGACCCGGGTGTCTTCC 510
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
311 TATTGTATTAATCTAGTGGCTATGCGCAGTGAAGAAAGAGGCTCGAGCCAAATTC 370
QY 511 GTCAGATAGTATCTGTGTGCTTATATGTGACAGCCAGGCTATGCTCAGAGGAACTCA 570
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
371 GCCAGATAGTGTCTGTGTGCTAGTCTGTCACCAAGAAAGTTTATTTGCTCATAGAGACTTAA 430
QY 571 AGCCAGAAATTTGCTGTTTGAATATCATATAATTAAGCTGATTGACTTTGGTCTCT 630
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 AGGCGAAACCTGCTTGGATGCTGATATGAACATCAAGATTGCAGACTTTTGGCTTCA 490
QY 631 GTCAGAAACCCAGGGTAAACAGGATTAACCATCTACAGACATGCTGTGGAGTCTGGCTT 690
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
491 GCAATGAATTC-----ACCTTTGGGAAACAGCTGGACACCTTCTGTGGCAGTCCCTT 544
QY 691 ATGACGACCTGATTAATAAAGGCAAAATCATATCTTGGATCAGAGGAGATGTTTGA 750
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
545 ATGCTGCCCAGAACTCTCCAGGCAAAAAATATGATGACCCGAGGTGATGTGTGA 604
QY 751 GCATGGGCATCTGTTATATGTTCTTATGTGTGATTTTACCATTTTGATGATGAATG 810
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
605 GCCTAGGAGTTATCCTCTATACACTGGTCAGCGGATCCCTGCTTTTGTGAGCAGAAC 664
QY 811 TAATGGCTTTATACAGAGATTTATGAGAG3AAAAATATGATGTTCCCAAGTGGCTCTCTC 870
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
665 TCAGAGAGCTGCGGACAGGCTACTGAGGGGAAATACCGTATTTCACTTACATGTCCA 724
QY 871 CCAGTAGCATTTTGTCTTTTCAAAATGCTGAGGTGGACCCAAAGAAACCGATTTCTA 930
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
725 CGGACTGTGAAAACCTGCTTAAGAAATTTCTCATTTCTTAATCCAGCAGAGAGGCATT 784
QY 931 TGAABAATCTATTGAACCATCCCTGGATCATGCAAGATTACAATCTATCTGTTGAGTGC 990
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
785 TAGAGCAAAATCATGAAGAATCGATGGATGAATGTGGGTACAGAGATGATGAATGAAC 844
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QY 991 AAAGCAAGAATCCTTTTATTACCTCGATGATGATTCGGTAAACAGAACTTTCTGTACATC 1050
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
845 CTTAGCTGGAGCACTCCTCTGACTACAAAGGACCCCGCGGACAGAGCTGATGGTGTCCA 904
QY 1051 ACAGAAACACAGGCAACAAATGGAGGATTTAAATTTCACTGTGGCAGTATGATCACTCA 1110
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
905 TGGGTTATACAGGGAAGAGATCCAGGACTCGCTGGTGGGCCAGAGATACAACGAGGTGA 964
QY 1111 CGGCTACCTATCTTCTGCTTCTAGCCAAGA 1140
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
965 TGGCCACCTATCTGCTCTCTGGGCTACAAGA 994

RESULT 7
US-09-949-016-1546
; Sequence 1546, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1546
; LENGTH: 2950
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1546

Query Match      8.0%; Score 197.6; DB 3; Length 2950;
Best Local Similarity 52.4%; Pred. No. 1.5e-43;
Matches 487; Conservative 0; Mismatches 434; Indels 9; Gaps 2;

QY 214 AAACATTTGGGACAGGTGGCTTTGCAAGGTCAAACTTGCCTGCCATATCCTTACTGGAG 273
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
478 AGACCATTTGGCAAGGTAATTTTGGCAAGGTGAAGTTGGCCCGACACATCCTGACTGGGA 537
QY 274 AGATGGTAGCTATAAAATCATGATTAACAAACACTAGGAGTGAATTTGGCCCGGATCA 333
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
538 AAGAGGTAGCTGTGAAGATCATTTGACAAAGACTCAACTGAACTCCCTCCAGCCCTCCAGAAC 597
QY 334 AAACG---GAGATTGAGGCCCTTGAAGAACTTGACACATCAGCATATATGTCAACTTACC 390
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
598 TATTCGCGAAGTAAGAATAATGAAGTTTGAATCATCCCAACATAGTAAATATTATTG 657
QY 391 ATGTGTAGACAGCCACAAATAATTTATGATGTTCTTGAGTACTGCCCTGGAGGAGC 450
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
658 AAGTGATTGAGACTGAGAAACGCTCTACTTGTCTATGAGTACGCTAGTGGCGGAGAGG 717
QY 451 TGTTTCACTATATAATTTCCAGGATGCGCTGTGCAAGAGGAGACCCGGGTGTCTTCC 510
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
718 TATTTGATTAACCTAGTGGCTCATGGCAGGATGAAGAAAGAGGCTCGAGCCAAATTC 777
QY 511 GTCAGATAGTATCTGCTGTGCTTATGTGCACAGCCAGGGCTATGTCTACAGGGACCTCA 570
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
778 GCAGATAGTGTCTGCTGTGCTGAGTACTGTACACAGAGTTTATTTGCTCATAGAGACTTAA 837
QY 571 AGCCAGAAATTTGCTGTTTGAATATCAATAATTAAGCTGATGATGCTTTGGTCTCT 630
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
838 AGGCGAAACCTGCTCTTGGATGCTGATGAACATCAAGATTGCAGACTTTGGCTTCA 897
QY 631 GTGCAAAACCCAGGGTAAACAGGATTAACCATCTACAGACATGCTGTGGAGTCTGGCTT 690
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
898 GCAATGAATTC-----ACCTTTGGGAAACAGCTGGACACCTTCTGTGGCAGTCCCCCTT 951
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US-09-984-890-1

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Query Match          7.9%; Score 196; DB 3; Length 2175;
Best Local Similarity 52.3%; Pred. No. 3.6e-43;
Matches 486; Conservative 0; Mismatches 435; Indels 9; Gaps 2;

QY 214 AAACATATTGGACACAGGTGGCTTTGCAAAAGCTCAAACTTGCTGCCATATCCTTACTTGGAG 273
DB 170 AGACCATTTGGCAGGGTAAATTTGCCAAGGTGAAGTTGGCCCGACACATCTCTGACTGGGA 229

QY 274 AGATGTAGCTATAAAATCATGGAATAAAACACACACTAGGGAGTGATTTGCCCGGATCA 333
DB 230 AAGAGGTAGCTGTGAAGATCATTTGACAGACTCAACTGNACTCCTCCAGCCTCCAGAAAC 289

QY 334 AAACG---GAGATTGAGGCTTTGAAAGAACCTTGAGACATCAGCATATATGTCAACTCTACC 390
DB 290 TATTCGCGAAGTGAAGATAATGAAGTTTGAATCATCCCAACATAGTTAAATATTATTTG 349

QY 391 ATGTGCTAGACAGCAGCAACAAATATTTCCAGAGTGGCTCTCAGAGAGGAGACCCGGGTTC 450
DB 451 TGTTTGAATATATATATATATATATATATATATATATATATATATATATATATATATATAT 510

QY 410 TATTTGATTACCTAGTGGCTCATGGCAGGATGAAGAAAGAGGCTCGAGCCAAATTC 469
DB 511 GTGAGATAGTATCTGTCTGTATATGTGTCACAGCCAGGGCTATGTCTACAGGGACCTCA 570

QY 470 GCCAGGTAGTGTCTGTGTCAGTACTGTCCAGAGTGGCTCTCAGAGAGGAGTAA 529
DB 571 ATGCGACCTGAGTTAATACAGGCAATCATATCTTGATCAGAGGAGGAGTTTGA 750

QY 631 GTGCAAAACCCAGGGTAAAGGATTACCATCTACAGACATGTGTGGAGTCTGGCTT 690
DB 590 GCAATGAATTC-----ACCTTTGGGAACAGCTGGAACCTTCTGTGGCAGTCCCGCTT 643

QY 691 ATGCGACCTGAGTTAATACAGGCAATCATATCTTGATCAGAGGAGGAGTTTGA 750
DB 644 ATGCTGCCCGCAGAACTCTTCCAGGGCAAAATATGATGGAACCGAGGTGGATGTGGA 703

QY 751 GCATGGGCATCTGTTTATATGTTTATGTTGGATTCTTACCATTTGATGATGATAATG 810
DB 704 GCCTAGGAGTTATCTCTTATACACTGGTTCAGCGGATCCCTGGCTTTTGTGACAGAAC 763

QY 811 TAATGCTTTATACAGGAAGATTATGAGAGGAAATATGATGTTCCCAAGTGGCTCTCTC 870
DB 764 TCAGAGAGCTGGGNAACGGGTACTGAGGGGAAATACCGTATTTCCATCTACATGTCCA 823

QY 871 CCAGTAGCATTTCTGCTTTCTTCAACAAATGCTGCAGGTGGACCCCAAGAAACGGAATTTCTA 930
DB 824 CGGACTGTGAAACCTGCTTTAAGAAATTTCTCAATCTTAATCCCAAGAGAGGAGCACTT 883

QY 931 TGAATAATCTATTTGAACCTCCCTGGATCATGCAAGATTACAACTATCCTGTTGAGTGGC 990
DB 884 TAGAGCAATCATGAAAGATTCGATGGATGAAATGTGGGTCAACGAAGATGATGAACCTAAAGC 943
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RESULT 10
US-10-274-194-1

```
; Sequence 1, Application US/10274194
; Patent No. 6706511
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE OF INVENTION: THERIOF
; FILE REFERENCE: CL001306DIV
; CURRENT APPLICATION NUMBER: US/10/274,194
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-274-194-1

Query Match          7.9%; Score 196; DB 3; Length 2175;
Best Local Similarity 52.3%; Pred. No. 3.6e-43;
Matches 486; Conservative 0; Mismatches 435; Indels 9; Gaps 2;

QY 214 AAACATATTGGACACAGGTGGCTTTGCAAAAGCTCAAACTTGCTGCCATATCCTTACTTGGAG 273
DB 170 AGACCATTTGGCAGGGTAAATTTGCCAAGGTGAAGTTGGCCCGACACATCTCTGACTGGGA 229

QY 274 AGATGTAGCTATAAAATCATGGAATAAAACACACACTAGGGAGTGATTTGCCCGGATCA 333
DB 230 AAGAGGTAGCTGTGAAGATCATTTGACAGACTCAACTGNACTCCTCCAGCCTCCAGAAAC 289

QY 334 AAACG---GAGATTGAGGCTTTGAAAGAACCTTGAGACATCAGCATATATGTCAACTCTACC 390
DB 290 TATTCGCGAAGTGAAGATAATGAAGTTTGAATCATCCCAACATAGTTAAATATTATTTG 349

QY 391 ATGTGCTAGACAGCAGCAACAAATATTTCCAGAGTGGCTCTCAGAGAGGAGACCCGGGTTC 450
DB 451 TGTTTGAATATATATATATATATATATATATATATATATATATATATATATATATATATAT 510

QY 410 TATTTGATTACCTAGTGGCTCATGGCAGGATGAAGAAAGAGGCTCGAGCCAAATTC 469
DB 511 GTGAGATAGTATCTGTCTGTATATGTGTCACAGCCAGGGCTATGTCTACAGGGACCTCA 570

QY 470 GCCAGGTAGTGTCTGTGTCAGTACTGTCCAGAGTGGCTCTCAGAGAGGAGTAA 529
DB 571 ATGCGACCTGAGTTAATACAGGCAATCATATCTTGATCAGAGGAGGAGTTTGA 750

QY 631 GTGCAAAACCCAGGGTAAAGGATTACCATCTACAGACATGTGTGGAGTCTGGCTT 690
DB 590 GCAATGAATTC-----ACCTTTGGGAACAGCTGGAACCTTCTGTGGCAGTCCCGCTT 643

QY 691 ATGCGACCTGAGTTAATACAGGCAATCATATCTTGATCAGAGGAGGAGTTTGA 750
DB 644 ATGCTGCCCGCAGAACTCTTCCAGGGCAAAATATGATGGAACCGAGGTGGATGTGGA 703

QY 751 GCATGGGCATCTGTTTATATGTTTATGTTGGATTCTTACCATTTGATGATGATAATG 810
DB 704 GCCTAGGAGTTATCTCTTATACACTGGTTCAGCGGATCCCTGGCTTTTGTGACAGAAC 763

QY 811 TAATGCTTTATACAGGAAGATTATGAGAGGAAATATGATGTTCCCAAGTGGCTCTCTC 870
DB 764 TCAGAGAGCTGGGNAACGGGTACTGAGGGGAAATACCGTATTTCCATCTACATGTCCA 823

QY 871 CCAGTAGCATTTCTGCTTTCTTCAACAAATGCTGCAGGTGGACCCCAAGAAACGGAATTTCTA 930
DB 824 CGGACTGTGAAACCTGCTTTAAGAAATTTCTCAATCTTAATCCCAAGAGAGGAGCACTT 883

QY 931 TGAATAATCTATTTGAACCTCCCTGGATCATGCAAGATTACAACTATCCTGTTGAGTGGC 990
DB 884 TAGAGCAATCATGAAAGATTCGATGGATGAAATGTGGGTCAACGAAGATGATGAACCTAAAGC 943
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QY 991 AAAGCAAGAAATCCTTTTATTTCACTCGATGATGATGCGTAACAGAACTTTCTGTATCATC 1050
DB 944 CTTACGTGGAGCACTCCCTGACTACAAGGACCCCGCGGACAGAGCTGATGGTGTCCA 1003
QY 1051 ACAGAAACACAGCGCAAAACAAATGGAGATTTAATTTTCACTGTGCGCATGATCACTCA 1110
DB 1004 TGGGTTATACACGGGAAGAGATCCAGATCGCTGGTGGGCCAGAGATACACAGAGTGA 1063
QY 1111 CGGCTACCTATCTTCTGCTTCTTAGCCAAGA 1140
DB 1064 TGGCCACCTATCTGCTCTGGGCTACAAGA 1093

RESULT 11
US-10-760-407-1
; Sequence 1, Application US/10760407
; Patent No. 6930173
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001306-DIV II
; CURRENT APPLICATION NUMBER: US/10/760,407
; CURRENT FILING DATE: 2004-01-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-760-407-1

Query Match 7.9%; Score 196; DB 3; Length 2175;
Best Local Similarity 52.3%; Pred. No. 3 6e-43;
Matches 486; Conservative 0; Mismatches 435; Indels 9; Gaps 2;

QY 214 AAACATATGGGACAGTGGCTTTGCAAGGTCAAACTTGCCTGCCATATCTTACTGGAG 273
DB 170 AGACCATTTGGCAAGGTAAATTTTGGCAAGTGAAGTTGGCCGACACATCTGACTGGGA 229
QY 274 AGATGGTACTATAAAATCATGGATTAACAAACACTAGGGAGTATTTGCCCGCGATCA 333
DB 230 AAGAGGTACTGTGAAGATCATTTGCAAGACTCAACTGAACCTCTCCAGCCTCCAGAAAC 289
QY 334 AAACG---GAGATTGAGGCTTTGAAGAACTTGAGACATCAGCATATATCTCACTTACC 390
DB 290 TATTCGGGAGTGAAGAAATGAAGGTTTGAATCATCCCAACATAGTTAAATTTTGG 349
QY 391 ATGTCTAGACAGCAGCAACAAATATTTCACTGTTCTTGAGTACTGCCCTGGAGGAGAGC 450
DB 350 AAGTGAATGAGACTGAGAAACGCTCTACTTGTCTATGAGTACGCTAGTGGCGGAGG 409
QY 451 TGTGTTGACTATATAATTTCCAGGATCGCTGTGCAAGAGGAGACCCGGGTGTTCTTCC 510
DB 410 TATTTGATTACCTAGTGGCTCATGGCAGGATGAAGAAAGAGGCTCGAGCCAAATTC 469
QY 511 GTCAGATAGTACTGCTGTTGTTTATGTGTCAGAGCCAGGCTATGCTCACAGGAGCTCA 570
DB 470 GCCAGTAGTGTCTGCTGTGCAAGTACTGTCAACAGAAATTTATGTCATAGAGACTTAA 529
QY 571 AGCCAGAAATTTGCTGTTTGTATGAATATATATAAATTAAGCTGATTTGACTTTGCTCT 630
DB 530 AGGCAGAAACCTGCTCTTGGATGCTGATGATGACATCAAGATTCAGAGCTTTGGCTTCA 589
QY 631 GTGCAAAACCCAGGGTAAACAGGATTAACATCTACAGACATGCTGTGGAGTCTGGCTT 690
DB 590 GCAATGAATTC-----ACCTTTGGGAACAAGCTGGACACCTTCTGTGGCAGTCCCTT 643
QY 691 ATGCAGCCTCAGTTTATACAGCAATATATCTTGGATCAGAGGACAGATGTTTGA 750
DB 644 ATGCTGCCCAAGAACTCTTCCAGGGGCAAAAATATGATGGACCCGAGGTGGATGTGGA 703

QY 751 GCAATGGGCATACCTGTTTATATGTTTATATGTTTATATGTTTATATGTTTATATGTTTATG 810
DB 704 GCCTAGAGCTTATCTCTATACACTGGTCAAGCGGATCCCTGCTTTTGTATGGACAGAAC 763
QY 811 TAATGCTTTTATACAGAAAGATTATGAGAGGAAATATGATGTTCCCAAGTGGCTCTCTC 870
DB 764 TCAAGGAGCTGGGGGACCGGTAAGTCTGAGGGGAAATATCCGTTATTCATTTCTACATGTCA 823
QY 871 CCAGTAGCATTTCTGCTTCTTCAACAAATCTGCGAGTGGACCCCAAGAAACGATTTCTA 930
DB 824 CGGACTGTGAACACCTGCTTTAGAAATTTCTCATTTTAAATCCACAGAGAGGCACTT 883
QY 931 TGAATAATCTATGAACCATCCCTGATCATGCAAGATTACAACTATCTGTTGAGTGGC 990
DB 884 TAGAGCAATCATGAAGATCGATGGTCAAGATGTTGGTCAAGAGATGATGAACATAAGC 943
QY 991 AAGCAAGAAATCTTTTATTTCACTCGATGATGATTCGTTACAGAACTTTCTGTATATC 1050
DB 944 CTTACGTGGAGCACTCTCCCTGACTACAAGGACCCCGCGGACAGAGCTGATGGTGTCCA 1003
QY 1051 ACAGAAACACAGGCAACAACTATGAGGATTTAAATTTCACTGTGGCAGTATGATCACCTCA 1110
DB 1004 TGGGTTATACACGGGAAGATCCAGGACTCCTGTTGGGCCAGAGATACACAGGAGTGA 1063
QY 1111 CGGCTACCTATCTTCTGCTTCTTAGCCAAGA 1140
DB 1064 TGGCCACCTATCTGCTCTGGGCTACAAGA 1093

RESULT 12
US-09-101-146-44
; Sequence 44, Application US/09101146
; Patent No. 6124125
; GENERAL INFORMATION:
; APPLICANT: Dartmouth College, St. Vincents Institute of
; APPLICANT: Medical Research, Kemp et al.
; TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PC
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/101,146
; FILING DATE: October 7, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PN7450
; FILING DATE: 8 JAN 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: DC-0050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (856) 810-1515
; TELEFAX: (856) 810-1454
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1647
; TYPE: Nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: No
US-09-101-146-44

Query Match 7.6%; Score 188.8; DB 3; Length 1647;
Best Local Similarity 57.2%; Pred. No. 3e-41;
Matches 365; Conservative 0; Mismatches 267; Indels 6; Gaps 1;

QY 330 ATCAAAACGGAGATTGAGGCGCTTGAAGAACCTGAGACATCAGCATATATGTCAACTCTAC 389
DB 181 ATCCGAGAGAGATCCAGAACCTGAGCTTTTCAGGCACCTCATATAATCAACTGTAC 240
QY 390 CATGCTAGAGACAGCCAAACAAATATTCATGCTTCTGAGTACTGCTCGGAGGAGAG 449
DB 241 CAGGTCATCAGTACACCGCTGATATTTTCATGCTGATGAAATATGCTCAGAGGAGAG 300
QY 450 CTGTTTGAATATATATTTCCAGGATCGCTCTCAGAGAGAGAGACCGGGTGTCTTC 509
DB 301 CTATTTGATATATCTGTAATAATGAAGGTTGAGACGAAAGAGAGTCACTGCTGTC 360
QY 510 CGTCAGATAGTATCTGCTGTTGCTTATGTCACAGCCAGGCTATGCTCAGAGGACCTC 569
DB 361 CAGCAGATCCTTCTGCTGCTGAGTATGTCACAGGATATGCTGCTCAGAGAGATTG 420
QY 570 AGCCAGAAAATTTGCTGTTGATGAAATATCATAAATTAAGCTGATTTGACTTTGCTTC 629
DB 421 AAACCTGAAAACGCTCCTGCTGCTGATGACACATGAAATGCAAGATAGCCGACTTCG 480
QY 630 TGTGCAAAACCCAGGTAACAGGATTAACATCTACAGACATGCTGTGGAGTCTGGCT 689
DB 481 T-----CAAATGATGTCAGATGCTGAAATTTTAAAGACGAGCTGTGCTGCCAAT 534
QY 690 TATGACGACCTGAGTTAATACAAAGCAATCAATCTTTGGATCAGAGGAGATGTTGG 749
DB 535 TATGCTGCACAGAGTAATTTTCAGGAGATTTCTACGAGGCTCTGAAGTAGACATCTGG 594
QY 750 AGCATGGCAATCTGTTATATGTTCTTATGTTGGAATTTCTACATTTGATGATGATTA 809
DB 595 AGCAGGGGGTCAATCTCTATGCTTGTGTTGGAATCTCTCCCTTTTGTATGATGACCA 654
QY 810 GTAAATGCTTTATACAGAGATTTATGAGGAAATATGATGTTCCCAAGTGGCTCTCT 869
DB 655 GTGCCAACTCTTTTAAAGAAATATGTCAGGGATATTTTATACCTCTAGATTTGAA 714
QY 870 CCAGTAGCATCTGCTTCTTCAACAAATGCTCAGGTGACCCCAAGAAACCGATTTCT 929
DB 715 CCCTCTGTAATAGCCTTTTGAAGCATATGCTCAGGTAGATCTTATGAAGAGGCCACA 774
QY 930 ATGAAAAATCTATTGAACCATCCCTGGATCATCAAGA 967
DB 775 ATAAAGATATCAGGGAACATGAATGTTTAAAGCAGA 812

RESULT 13
US-08-557-006C-37
; Sequence 37, Application US/08557006C
; Patent No. 6258547
; GENERAL INFORMATION:
; APPLICANT: Beri, Rajindar K.
; APPLICANT: Carling, David
; APPLICANT: Forster, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NGAP/PHM37588/UST
; CURRENT APPLICATION NUMBER: US/08/557,006C
; CURRENT FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: PCT/GB94/01093
; PRIOR FILING DATE: 1994-05-20
; PRIOR APPLICATION NUMBER: GB 9310489.1
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: GB 9318010.7
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 37
; LENGTH: 1736
; TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rat liver AMP
; OTHER INFORMATION: protein kinase
US-08-557-006C-37

Query Match 7.6%; Score 188.6; DB 3; Length 1736;
Best Local Similarity 54.5%; Pred. No. 3.5e-41;
Matches 427; Conservative 0; Mismatches 344; Indels 12; Gaps 2;

QY 193 TCAAATATATGAAATACATGAAACTATTTGGACAGGTGGCTTTTCAAGGTCAAACTTG 252
DB 38 TCGGACACTACGTGCTGGCGCACCGCTGGCGCTCGGCACCTTCGGCAAGTGAAGATTG 97
QY 253 CCGTCATATCTTACTTGGAGAGATGGTAGCTATATAAATCATGTATAAAAACACACTAG 312
DB 98 GAGAACATCAATTACAGGCCATAAAGTGGCAGTTAAATCTTAAATAGACAGAGATTTC 157
QY 313 GGAG-----TGATTTGCCCGGATCAAAAACCGAGATTGAGGCCTTTGAAGAACCTTGAGAC 366
DB 158 GCAGTTTAGATGTTGTTGGAAAAATAAAAACGAGAAATTCAAAAATCTTAAACTCTTTCGTC 217
QY 367 ATCAGCATATATGCTCAACTCTACCATGTCTAGACAGCAGCCAAACAAATATTCATGGTTC 426
DB 218 ATCTCTCATATTAACAACCTATACAGGTGATCAGCACTCCAAACAGATTTTTTATGGTAA 277
QY 427 TTGAGTACTGCCCTCGAGGAGAGCTGTTTGACTATATAATTTCCAGGATCGCCTGTCTAG 486
DB 278 TCGAATATGCTGTGAGGTGAAATTTTATGACTACATCTGTAAAGCATGAGCGGTTGAAG 337
QY 487 AAGAGGAGACCCGGGTGTTCTTCCTCAGATAGTATCTGCTGTGCTTATGTCACAGCC 546
DB 338 AGATGGAAGCAGCGGCTCTTTCAGCAGATCTGCTGCTGTGATTACTGTCTATAGGC 397
QY 547 AGGGCTATGCTCAGAGGACCTCAAGCCAGAAAAATTTGCTGTTGATGATATCATATAAT 606
DB 398 ATATGTTGTTTCATCGAGACCTGAAACCGAGAAATGTCTCTGTGATGCACATGAATG 457
QY 607 TAAAGCTGATTGACTTTTGGTCTCTGTGCAAAACCCAGGGTAAACAGGATTAACCATCTAC 666
DB 458 CCAAGATAGCCGATTTCCGATTAATCT-----AATATGATGTCAGATGGTGAATTTCTGA 511
QY 667 AGACATGCTGTGGAGTCTGGCTTATGACGACCTGAGTTAATACAGCAAAATCATATC 726
DB 512 GAACTAGTTGCGGATCTCCAAATTTATGACGACCTGAAAGTCATCTCAGGCAGATTTGATG 571
QY 727 TTGGATCAGAGCAGATGTTTGGAGCATGGGCATCTGTTATATATGTTCTTATGTTGGAT 786
DB 572 CAGGTCCTGAAGTTGATATCTCGAGCTGTGGTGTATCTTTGATGCTCTCTTTTGGCA 631
QY 787 TTCTACCATTTGATGATGATAATGTAATGGCTTTTATACAAAGAGATTAATGAGAGAAAA 846
DB 632 CCCTCCATTTGATGATGAGCATGTACCTACGTTATTTAAGAGATCCGAGGGGTGTCT 691
QY 847 ATGATGTTCCCAAGTGGCTCTCTCCAGTAGCATTTCTGCTTTCACAAAATGCTCAGG 906
DB 692 TTATATATCCAGATATCTCAATGCTTGTGCGCACTCTCCTGATGATATGCTCAGG 751
QY 907 TGGACCCCAAGAAACGGATTTCTATGAAAAATCTATTGAACCATCCCTGGATCATGCAAG 966
DB 752 TTGACCCACTGAAACGAGCACTATCAAAAGACATAGAGAGCATGAATGTTTAAACAAG 811
QY 967 ATT 969
DB 812 ATT 814

RESULT 14
US-08-557-006C-36
; Sequence 36, Application US/08557006C
; Patent No. 6258547
; GENERAL INFORMATION:
; APPLICANT: Beri, Rajindar K.

:	APPLICANT:	Carling, David			
:	APPLICANT:	Forder, Robert A.			
:	TITLE OF INVENTION:	NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE			
:	FILE REFERENCE:	NCAP/PHM37588/UST			
:	CURRENT APPLICATION NUMBER:	US/08/557,006C			
:	CURRENT FILING DATE:	1996-03-06			
:	PRIOR APPLICATION NUMBER:	PCT/GB94/01093			
:	PRIOR FILING DATE:	1994-05-20			
:	PRIOR APPLICATION NUMBER:	GB 9310489.1.			
:	PRIOR FILING DATE:	1993-05-21			
:	PRIOR APPLICATION NUMBER:	GB 9318010.7			
:	PRIOR FILING DATE:	1993-08-31			
:	NUMBER OF SEQ ID NOS:	44			
:	SOFTWARE:	PatentIn Ver. 2.1			
:	SEQ ID NO	36			
:	LENGTH:	1783			
:	TYPE:	DNA			
:	ORGANISM:	Human AMP protein kinase			
:	US-08-557-006C-36.				
<hr/>					
	Query Match	7.6%	Score 188.6;	DB 3;	Length 1783;
	Best Local Similarity	54.5%	Pred. No. 3.5e-41;		
	Matches 427;	Conservative 0;	Mismatches 344;	Indels 12;	Gaps 2;
<hr/>					
Qy	193	TCAAAATATTGAATTACATAAAGTATTTGGGACAGGTGGCTTTGGCAAAGTGTAACCTTTG	252		
Db	39	TCGGACACTAGTGTCTGGCGGCACACGCTGGCGCTCGGCACCTTTCCGCCAAAGTGAAGATTG	98		
Qy	253	CCTGCCATATCTTTACTTGGAGAGATGTTAGCTATAAAAATCATGGATAAAAAACACACATAG	312		
Db	99	GAGAACAATCAATTAACAGGCCATAAAGTGGCAGTTTAAATCTTAAATAGACAGAAGATTC	158		
Qy	313	GGAG-----TGATTTGGCCCCGGGATCAAAACGGAGATTGAGGCCCTTGAAGAACCTGAGAC	366		
Db	159	GCAGTTTAGATGTTGTTTGGAAAAATAAAACGAGAAATTCAAAATCTTAAACTCTTTTCGTC	218		
Qy	367	ATCAGCATATATGTCAACTCTTACCATGTGCTAGAGACAGCCAAACAAATATTCATGTGTTTC	426		
Db	219	ATCCTCATATATCAAACTATACCAGGTGATCAGCACCTCCAACAGATTTTTTTTATGGTAA	278		
Qy	427	TTGAGTACTGCCCTGGAGGAGAGCTGTTTGACTATATAATTTCCACAGATCGCCCTGTCAG	486		
Db	279	TGGAATATGTCTGGAGGTGAATATTATTGACTACATCTGTAAGCATGGACGGGTTGAAG	338		
Qy	487	AAGAGGAGACCCGGGTTGTCTTCCTCGTCAGATAGTATCTGCTGTTGCTTATGTGACAGCC	546		
Db	339	AGATGGAAAGCCAGCGCGCTCTTTCAGCAGATCTGCTGCTGTGATTACTGTCTATAGGC	398		
Qy	547	AGGECTATGCTCAAGGAGCTCAAGCCAGAAAATTTGCTGTTTGTATGAATATCATAAAT	606		
Db	399	ATA TGGTTGTTCA TCGAGACCTGAAAC CAGAGAATGT CCTGTGGATG CACACATGAATG	458		
Qy	607	TAAAGCTGATTGACTTTTGGTCTCTGTGCAAAACCAAGGGTAA CAGAGATTACCATCTAC	666		
Db	459	CCAAGATAGCCGATTTTCGGATTAATCT-----AATATATGATGTCAATGGTGAATTTCTGA	512		
Qy	667	AGACATGCTGTGGAGTCTGGCTTATG CAGCACCTCGATTGTTAAATCAAGGCCAAATCATATC	726		
Db	513	GAACTAGTTGGGATCTCCAAATTTATG CAGCACCTGAACTCAAGTCATCTCAGGCAGATTGTATG	572		
Qy	727	TTGGATCAGAGGCAGATGTTTGGAGCATGGGCATAC TGTTATATGTTTCTTATGTGTGGAT	786		
Db	573	CAGGTCTGGAAGTTGATATCTGGAGCTGTGGTGTATCTTTGTA TGCTCTCTTTTGTGCA	632		
Qy	787	TTCTACCATTTGATGATATAATGTAATGGCTTTTATACAGAGAATATATGAGAGAAAT	846		
Db	633	CCCTCCCATTTGATGATGAGCATGTAC TAGTTTATTTAAGAGATCCGAGGGGGTGCTCT	692		
Qy	847	ATGATGTTTCCCAAGTGGCTCTCTCCAGTAGCATTTCTGCTTCTTCAACAATGCTGCAGG	906		
Db	693	TTTATATFCCCAGAAATATCTCAATCGTTCTGTGCGCACTCTCCTGATGCATATGCTGCAGG	752		
Qy	907	TGGACCCAAAGAACCGGATTTCTATGAAAAATCTATTGAAACCATCTCCTGGATCATGCAAG	966		

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Db      753  TTGACCCACTGAAACGAGCAACTATCAAAAGACATGAAGAGCATGAATGGTTTAAACAAG 812
      967  ATT 969
      813  ATT 815

RESULT 15
US-09-949-016-1699
; Sequence 1699, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1699
; LENGTH: 2210
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1699

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Query Match	7.3%	Score 181.2;	DB 3;	Length 2210;
Best Local Similarity	56.4%;	Pred. No. 4.2e-39;		
Matches 361;	Conservative 0;	Mismatches 273;	Indels 6;	Gaps 1;
Qy	330	ATCAAAACGAGATTGAGGCGTTTGAGAACTCTGAGACATCAGCATATATGTCAACTCTAC	389	
Db	89	ATAAACGAGAAATTCAAATCTATAAACTCTTTGTCATCTCATATATATCAAACTATAC	148	
Qy	390	CATGTGCTAGAGACAGCCAAACAAAATATTATCATGGTTCTTGAGTACTGCCCTGGAGGAGAG	449	
Db	149	CAGGTGATCAGCACTCCAAACAGATTTTTTTATGGTAATGGAATATGTGTCGAGAGGTGAA	208	
Qy	450	CTGTTTGACTATATATAATTTCCAGGATCGCCTGTCAAGAGAGAGACCCGGGTTGTCTTC	509	
Db	209	TTATTTTGACTATCATCTGTAAAGCATGGAACGGGTTGAAGAGATGGAAGCAACGCGGCTCTTT	268	
Qy	510	CGTCAGATATGATCTGCTGTTGCTTATGTGCACAGCCAGGGCTATGCTCACAGGGACCTC	569	
Db	269	CAGCAGATTCGTCTGCTGTGGATTACTGTCAATAGGCATATGGTTGTTTCATCGAGACCTG	328	
Qy	570	AAGCCAGAAATTTGCTGTTTGATGTAATCATATAAATATAAGCTGATPGACTTTGGTCTC	629	
Db	329	AAACCAGAGAAATGTCCTGTTGGATGACACATCAATGSCCAAGATAGCCGATTTCCGATTA	388	
Qy	630	TGTGCAAAACCCAAAGGTAACAAGATTACCATCTACAGACATGCTGTGGAGTCTGGCT	689	
Db	389	TCT-----AATATGATGTCAGATGGTGAATTTCTGAGAACTATGTTGCGGATCTCCAAT	442	
Qy	690	TATGACGACCTCAGTTTAATCAAGGCAAAATCATATCTTCGGATCAGAGGCAGAGATGTTGG	749	
Db	443	TATGACGACCTGAATCATCTCAGGCAGATTGTATGCGAGTCTGAAATTGATATCTGG	502	
Qy	750	AGCATGGGCATCTGTTTATATGTTCTTATGTGTGGATTCTTACCAATTTGATGATGAAT	809	
Db	503	AGCTGTGGTGTATCTTGATGTCCTCTTTGTGGCAACCTCCCAATTTGATGATGAGCAT	562	
Qy	810	GTAATGCTTTTATCAAGAAAGATTATGAGAGGAAAATATGATGTTTCCCAAGTGGCTCTCT	869	
Db	563	GTACTCTACGTTATTTAAGAAAGATCCGAGGGGGTGTCTTTTATATCCAGAAATATCTCAAT	622	

Qy	870	CCAGTAGCATTCTGCTTCTTCAACAAATGCTGAGGTGGACCCAAAGAAACGGATTCT	929
Db	623	CGTTCTGTGCCCACTCTCTCTGATGCATATGCTGAGGTGACCCACTGAAACGAGCAACT	682
Qy	930	ATGAAAAATCTATTGAACCATCCCTGGATCATGCAAGATT	969
Db	683	ATCAAGACATAAGAGAGCATGAATGGTTTAAACAAGATT	722

Search completed: November 21, 2006, 19:46:41
Job time : 463 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2006, 19:34:26 ; Search time 11521 Seconds
(without alignments)
11988.608 Million cell updates/sec

Title: US-10-656-598-1
Perfect score: 2470
Sequence: 1 tggcgggcggaagcgcca.....ataaacaccatttgtgaatat 2470

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est3:*

3: gb_est4:*

4: gb_est5:*

5: gb_est6:*

6: gb_hic:*

7: gb_est2:*

8: gb_est7:*

9: gb_est8:*

10: gb_est9:*

11: gb_gss1:*

12: gb_gss2:*

13: gb_gss3:*

14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1615	65.4	1615	6	CR605252	CR605252 full-length
2	1548.8	62.7	2469	6	AK145021	AK145021 Mus muscu
3	1543.4	62.5	2430	6	AK145316	AK145316 Mus muscu
4	1543.4	62.5	2914	6	AK011932	AK011932 Mus muscu
5	1541.8	62.4	2447	6	AK167457	AK167457 Mus muscu
6	1541.8	62.4	2489	6	AK164138	AK164138 Mus muscu
7	1535.8	62.2	2541	6	AK161029	AK161029 Mus muscu
8	1525.8	61.8	2396	6	BC020416	BC020416 Mus muscu
9	1521.4	61.6	2559	6	AK137000	AK137000 Mus muscu
10	1520.4	61.6	2488	6	AK010498	AK010498 Mus muscu
11	1368	55.4	1956	14	DQ048096	DQ048096 Homo sapi
12	1036.4	42.0	1096	1	AL577157	AL577157 AL577157
13	1020.6	41.3	1030	1	AL554470	AL554470 AL554470
14	872.4	35.3	1091	3	BM928784	BM928784 AGENCOURT
15	859	34.8	1898	14	DQ048097	DQ048097 Pan trogl
16	834.8	33.8	855	2	BM471174	BM471174 AGENCOURT
17	830.6	33.6	901	1	AU130934	AU130934
18	822.6	33.3	960	2	BG682772	BG682772 602651263
19	813.2	32.9	852	1	AU124892	AU124892 602731280

20	792.6	32.1	1007	3	BQ64763	BQ64763 AGENCOURT
21	781	31.6	854	1	AU124737	AU124737
22	778	31.5	1006	3	BM927868	BM927868 AGENCOURT
23	770.6	31.2	945	3	BQ650221	BQ650221 AGENCOURT
24	756	30.6	762	9	CX872457	CX872457 HESCA_69
25	744.6	30.1	803	2	RI086933	RI086933 602850361
26	743.2	30.1	754	1	AU130717	AU130717
27	735.8	29.8	839	1	AI693521	AI693521 w43e08.x
28	735.2	29.8	848	3	BQ221427	BQ221427 AGENCOURT
29	735.2	29.8	1034	2	BG396052	BG396052 602458792
30	733	29.7	734	4	BX105144	BX105144 BX105144
31	726.4	29.4	750	3	BU595645	BU595645 AGENCOURT
32	720.4	29.2	806	2	BG105946	BG105946 602290134
33	715.8	29.0	882	1	AA767453	AA767453 n282d06.s
34	714.8	28.9	746	4	CA426797	CA426797 UI-H-FE1-
35	710.6	28.8	760	4	CA749050	CA749050 UI-H-FE1-
36	700	28.3	818	9	DR155628	DR155628 HESCA_56
37	699.8	28.3	862	7	BE881704	BE881704 601485932
38	690.4	28.0	772	2	BG683434	BG683434 602651263
39	682.8	27.6	714	4	CA310724	CA310724 UI-CF-FN0
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41	681.4	27.6	733	2	BG286546	BG286546 602382548
42	679.2	27.5	853	8	CV800888	CV800888 AGENCOURT
43	678.8	27.5	715	3	BU622206	BU622206 UI-H-PH1-
44	660	26.7	672	8	CN307609	CN307609 328781381
45	654.8	26.5	890	2	BG752315	BG752315 602731280

ALIGNMENTS

RESULT 1
CR605252
LOCUS
DEFINITION
full-length cDNA clone CSODI084YI07 of Placenta Cot 25-normalized of Homo sapiens (human).
ACCESSION
CR605252
VERSION
CR605252.1 GI:50486059
KEYWORDS
HTC; CDSLT cDNA.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1615)
AUTHORS
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
REMARK
Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
REFERENCE
2 (bases 1 to 1615)
AUTHORS
Genoscope.
TITLE
Direct Submission
JOURNAL
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="CSODI084YI07"
/tissue type="Placenta Cot 25-normalized"
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Query Match 65.4%; Score 1615; DB 6; Length 1615;

	Best Local Similarity	100.0%; Pred. No. 0;	Matches 1615; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Dd	1	GCCCGCTCTCAGGACAGCAGGCCCTGTCTTCTGTGGGCGCGCTCAGCCGTGCC	60
Qy	121	TCCGCCCTCAGGTTCTTTTTCTAATTCCAAATAAACTTGCAAGAGCATATGAAGAATT	180
Dd	61	TCCGCCCTCAGGTTCTTTTTCTAATTCCAAATAAACTTGCAAGAGCATATGAAGAATT	120
Qy	181	ATGATGAACCTTCAAAATATATGAAATCATGAAACTATTTGGGACAGGTGGCTTTCCAA	240
Dd	121	ATGATGAACCTTCAAAATATATGAAATCATGAAACTATTTGGGACAGGTGGCTTTGCAA	180
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Dd	181	AGGTCAAACTTGCCTGCCATATCTTA CTGAGAGATGGTAGCTATAAAAATCATGGATA	240
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Dd	241	AAAACACATAGGAGTGATTTGGCCCGGATCAAAACGGAGATGGAGCCTTGAAGAACC	300
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Dd	301	TGAGACATCAGCATATATGTCAA CTCTACCATGTGCTTAGAGACAGCCAACAAATATATCA	360
Qy	421	TGGTTCTTGAGTACTGCCCTGGAGGAGCTGTTTGACTATATAATTTCCCAGGATGCC	480
Dd	361	TGGTTCTTGAGTACTGCCCTGGAGGAGCTGTTTGACTATATAATTTCCCAGGATGCC	420
Qy	481	TGTCAGAAGAGGAGACCCGGGTGTCTTCCGTCAAGATAGTATCTGCTGTGCTTATGTGC	540
Dd	421	TGTGAGAAGAGGAGACCCGGGTGTCTTCCGTCAAGATAGTATCTGCTGTGCTTATGTGC	480
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Dd	481	ACGCCAGGGCTATGCTCA CAGGACCTCAAGCCAGAAATTTGCTGTTTGATGAATATC	540
Qy	601	ATAAATTAAGCTGATTTGACTTTGGTCTCTGTGCAAAACCCAAAGGTAAACAAGGATTACC	660
Dd	541	ATAAATTAAGCTGATTTGACTTTGGTCTCTGTGCAAAACCCAAAGGTAAACAAGGATTACC	600
Qy	661	ATCTACAGACATGCTGTGGGAGTCTGGCTTATGCAGCACCTTGAGTTAATAACAAGGCAAT	720
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Dd	661	CATATCTTGGATCAGAGCAGATGTTTGGAGCATGGGCATAC TGTATATGTTCTTATGT	720
Qy	781	GTGGATTTCTACATNTTGATGATTAATGTAATGGCTTTTATACAAGAGATATAGAG	840
Dd	721	GTGGATTTCTACATNTTGATGATTAATGTAATGGCTTTTATACAAGAGATATAGAG	780
Qy	841	GAAATATGATGTTTCCAAAGTGGCTCTCTCCAGTAGCATTTCTGCTTCTTCAACAAATGC	900
Dd	781	GAAATATGATGTTTCCAAAGTGGCTCTCTCCAGTAGCATTTCTGCTTCTTCAACAAATGC	840
Qy	901	TGCAGGTGGACCCAAAGAACCGGATTTCTATGAAAAATCTATTGAAACCATCCCTGGATCA	960
Dd	841	TGCAGGTGGACCCAAAGAACCGGATTTCTATGAAAAATCTATTGAAACCATCCCTGGATCA	900
Qy	961	TGCAAGATTACAACTATCTGTTGAGTGGGAAAGCAGAGATCCCTTTTATTCACCTCGATG	1020
Dd	901	TGCAAGATTACAACTATCTGTTGAGTGGGAAAGCAGAGATCCCTTTTATTCACCTCGATG	960
Qy	1021	ATGATTGGGTAA CAGAACTTTCTGTACATCAGAGAA CAA CAGGCAACCAATGAGGATT	1080
Dd	961	ATGATTGGGTAA CAGAACTTTCTGTACATCAGAGAA CAA CAGGCAACCAATGAGGATT	1020
Qy	1081	TAATTTTCACTGTGGCAGTATGATCACTCAGGGCTACTATTTCTTCTGTCTTAGCCCAAGA	1140

[illegible]

TITLE JOURNAL PUBLISHED REFERENCE AUTHORS	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 11076861
	4
	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., De Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohetsuki, S. and Hayashizaki, Y.
	RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium Nature 409 (6821), 685-690 (2001) 11217851
CONSTRM JOURNAL PUBLISHED REFERENCE AUTHORS	5 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Brad, D., Bruscia, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Kawaji, H., Kasukawa, Y., Kedzierzki, R.M., King, B.L., Konagaya, A., Kustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okado, T., Pavan, W.J., Perte, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylot, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kigawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y. FANTOM Consortium Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420 (6915), 563-573 (2002) 12466851
	6
	Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shinkawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E., Ambesi-Impombato, A., Apweiler, R., Aturaliya, R.N., Bailey, T.L., Bansal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Crome, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagioli, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M.,
CONSTRM JOURNAL PUBLISHED REFERENCE AUTHORS	Georgii-Hemming, P., Giegeras, T.R., Gojobori, T., Green, R.E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Huminecki, L., Iacono, M., Ikeo, K., Iwano, A., Ishikawa, T., Jakt, M., Kanapin, A., Kato, M., Kawasawa, Y., Kelsa, J., Kitamura, H., Kitano, H., Kollias, G., Kriehnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Liu, S., McWilliam, S., Madan, Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakauchi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohata, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavese, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Rost, B., Ruan, F., Salzberg, S.L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semple, C.A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugita, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamanishi, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Bruscia, V., Quackenbush, J., Wahlstedt, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watahiki, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y. FANTOM Consortium The transcriptomic landscape of the mammalian genome Science 309 (5740), 1559-1563 (2005) 16141072
	7
	Kasukawa, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yagi, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sandelin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlstedt, C. RIKEN Genome Exploration Research Group Antisense transcription in the mammalian transcriptome Science 309 (5740), 1564-1566 (2005) 16141073
	8 (bases 1 to 2469) Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan [E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216] cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ Location/Qualifiers 1. .2469 /organism="Mus musculus" /mol_type="mRNA" /db_xref="FANTOM DB:G830026003" /db_xref="taxon:10090" /clone="G830026003"
CONSTRM JOURNAL PUBLISHED REFERENCE AUTHORS	COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ Location/Qualifiers 1. .2469 /organism="Mus musculus" /mol_type="mRNA" /db_xref="FANTOM DB:G830026003" /db_xref="taxon:10090" /clone="G830026003"
	FEATURES source

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CDS

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ASPTREPAPAKAOCLREAPVPTPCNSAGADTLTTGVI SPERRCHRMVDVINOAHME
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Query Match 62.7%; Score 1548.8; DB 6; Length 2469;

Best Local Similarity 80.7%; Pred. No. 0;

Matches 1910; Conservative 0; Mismatches 417; Indels 41; Gaps 7;

QY	112	GCGTGCCTCCGCGCTCAGGTTCTTTTCAATTC	791	TGCTCATGTGTGGATTTCTTCA
DB	71	GCGGCGCGCTCCCTTCCAGTTCTGGTTGTCT	832	TTATGAGAGGAAAATATGATGTTCCCAAGTG
QY	172	TGAAGATTATGATGAATCTTCAATATATTCA	791	TAATGAGAGGAAAATACGAGTTCTTAAGTG
DB	131	TGAAGATTATGAGAACTCTCAATATCTAGAC	892	AAACAAATGCTCAGGTGGACCCCAAGAAAC
QY	232	GCTTTGCAAGGTCAAACTTGCCTGCCATATC	851	AGCAGATGTTGTCAGGTGGACCCCAAGAAAC
DB	191	GCTTTGCAAGGTCAAACTGCGCTGCCATGTC	952	CCTGGATCATGCAAGATTACAATCTATCCT
QY	292	TGATGATATAAACAACATGAGGATGATTTG	911	CCTGGGTCTATGCAAGATTACAGTGTCC
DB	251	TCATGATTAAGAAATGCGCTAGGAGTGAAT	1012	ACCTCGATCATGATTCGCTAACAGAACTTT
QY	352	TGAAGAACCTTGACATATGATATGCTACCA	971	ACCTCATGAGGATTTGCGTGACAGAGCTTT
DB	311	TGAAGAGTCTGAGACACGACATATGTCACT	1071	TGGAGGATTTAATTTCACTGTGGCAGTATG
QY	412	AAATATTATGTTTCTTGATGACTGCGCTTG	1131	TAGCCAAAGAGGCTCGGGGAAAACAGTTC
DB	371	AAATATTATGTTTCTTGAGTACTGCTTGAG	1090	TGGAGGATTTAATTTTCGTGCTGCGAGTA
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DB	431	AGGATCGCTGTGCGAAGAGGAGACCGGGTG	1150	TAGCCAAAGAGGCTCGGGGAAAACAGTTC
QY	532	CTTATGTGACACGCGGGCTATGCTCACAGG	1251	AAGCCAGTGTCTACCCCATTCACAGACAT
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QY	592	ATGAATATCAATAATTAAAGCTGATTTGAT	1311	CGCAAGTGATAAAAATTTATGTGGCGGGA
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QY	651	AGGATACCATCTACAGACATGCTGTGGAGT	1371	TATCAACAGGTGCTGTACTCTCCCGAAAT
DB	611	AGGATACCATCTGCGACAGTGTGTGGAGC	1306	TATTA-----GCTCCAAAGACGCCACA
QY	712	AAGGCAAAATCATATCTTGGATCAGAGCAG	1431	ATGGGTGGAAATCTAAATCATTTAACTCC
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QY	772	TTCTTATGTGTGGATTTCTACCAATTTGAT	1491	AGAACAAAGAAATGTATATCTCTTAAGT
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Db	1907	AGTCTGATTTTGGCAAGTGCACAAATGCAATTTGAAATTTAGAAAGTGTGCACGTTCAAACAC	1966
QY	2032	CCGATGTGGTGGTATCAGGAGCAGCGGCTTAAAGGCGATGCTGGGTTTACAAAAGAT	2091
Db	1967	CTGACGTGTGTAGGCATCCGAGACAGCGGCTGAAGGGTGTGCTGGTTTACAGAGAT	2026
QY	2092	TAGTGGAGACATCTATCTAGCTGCAAGTATAATTTGATGGAATTTCTCCATCTGCGCG	2151
Db	2027	TAGTGGAGATATCTTGTCTGGCTGCAAGATGTGACCGATGACAGATGTGCGCTGCGCGG	2086
QY	2152	ATCAGTGTGGTGTGATACAGCCTACATAAAGACTGTATGATCGCTTGTGATTT-----	2204
Db	2087	ATGAATGTGGTGTGATGCTGCACAGGAGAACTCTGGAATTTGCTTCAATTTGGGGGCC	2146
QY	2205	TTAAAGTTCAATGGAACCTACCAACTTGTGTTTCTAAAGAGCTATCTTAAAGACCAATATCTCT	2264
Db	2147	CATTGATCTATGGAACCTACAGCTCATTTAAATAGCCATCTTCAAGACCAATGTATTT	2206
QY	2265	TTGTTTAAACAAAAGATATTTTGTGTATGAATCTAAATCAAGCCCATCTGTCAAT	2324
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QY	2325	AT--GTTACTGCTTTTAAATCATGTTGGTTTGTATATAATTAATTTGATCTTTCTTA	2382
Db	2266	ATCAATTAATCTCTGTTTAAATCATG--GGCTGGTATGTTAGTAACTG-----TTTTTA	2318
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AKI45316			
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DEFINITION	Mus musculus 4 cells embryo 4 cells cDNA, RIKEN full-length enriched library, clone:10C001106 product:maternal embryonic leucine zipper kinase, full insert sequence.		HTC 21-SEP-2005
ACCESSION	AKI45316		
VERSION	AKI45316.1	GI:74208326	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
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REFERENCE	1		
AUTHORS	Carninci, P. and Hayaishizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
PUBLISHED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayaishizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
PUBLISHED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,		

QY	1912	TTCTTCCAAAGAGCATGTTGACTTTTGTACAAAAGGGTTTATACACTGAAGTGTCAAACAC	1971
Db	1847	TTCTTCCAAAGAGAAATGTGGACTTCGTACAGAAAGTTTACACACTAAAGTGTCAAACGC	1906
QY	1972	AGTCAGATTTTGGGAAAGTCACAAATGCAATTTGAAATTTAGAAAGTGTGCACGTTCAAACAC	2031
Db	1907	AGTCTGATTTTGGCAAGTGCACAAATGCAATTTGAAATTTAGAAAGTGTGCACGTTCAAACAC	1966
QY	2032	CCGATGTGGTGGTATCAGGAGCAGCGGCTTAAAGGCGATGCTGGGTTTACAAAAGAT	2091
Db	1967	CTGACGTGTGTAGGCATCCGAGACAGCGGCTGAAGGGTGTGCTGGTTTACAGAGAT	2026
QY	2092	TAGTGGAGACATCTATCTAGCTGCAAGTATAATTTGATGGAATTTCTCCATCTGCGCG	2151
Db	2027	TAGTGGAGATATCTTGTCTGGCTGCAAGATGTGACCGATGACAGATGTGCGCTGCGCGG	2086
QY	2152	ATCAGTGTGGTGTGATACAGCCTACATAAAGACTGTATGATCGCTTGTGATTT-----	2204
Db	2087	ATGAATGTGGTGTGATGCTGCACAGGAGAACTCTGGAATTTGCTTCAATTTGGGGGCC	2146
QY	2205	TTAAAGTTCAATGGAACCTACCAACTTGTGTTTCTAAAGAGCTATCTTAAAGACCAATATCTCT	2264
Db	2147	CATTGATCTATGGAACCTACAGCTCATTTAAATAGCCATCTTCAAGACCAATGTATTT	2206
QY	2265	TTGTTTAAACAAAAGATATTTTGTGTATGAATCTAAATCAAGCCCATCTGTCAAT	2324
Db	2207	TGCTTTTCAACAAAAATTTTACTTTTGGCTGAATCCCAAGCAA-CTGTTCTGTCAAT	2265
QY	2325	AT--GTTACTGCTTTTAAATCATGTTGGTTTGTATATAATTAATTTGATCTTTCTTA	2382
Db	2266	ATCAATTAATCTCTGTTTAAATCATG--GGCTGGTATGTTAGTAACTG-----TTTTTA	2318
QY	2383	GATTCACCTCCATATGTAATGTAAGCTCTTAATATGCTCTTTGTAATGTTGAATTTTC	2442
Db	2319	TATTCATCTCCATCAGGGATGCCGCTCTTCACTGTGACTCATTTGATGTACAGTTTC	2378
QY	2443	TTTCTGAATAAAACCATTTGTGAATAT	2470
Db	2379	TTTCTGAACATAAAACCATTTGTGAATAT	2406
RESULT 3			
AKI45316			
LOCUS	2430 bp	mRNA	linear
DEFINITION	Mus musculus 4 cells embryo 4 cells cDNA, RIKEN full-length enriched library, clone:10C001106 product:maternal embryonic leucine zipper kinase, full insert sequence.		HTC 21-SEP-2005
ACCESSION	AKI45316		
VERSION	AKI45316.1	GI:74208326	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.		
REFERENCE	1		
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TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
PUBLISHED	10349636		
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AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayaishizaki, Y.		
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Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

11076861

4

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, Y., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gajobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleschmann, W., Gaasterland, T., Glessi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsumoto, Y., Nakaide, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, J., Sakamoto, N., Sakaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S. and Hayashizaki, Y.

RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

11217851

5

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FANTOM Consortium

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420 (6915), 563-573 (2002)

12466851

6

Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M. C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V. B., Brenner, S. E., Batalov, S., Forrest, A. R., Zavolan, M., Davis, M. J., Wilming, L. G., Aidinis, V., Allen, J. E., Ambesi-Impombato, A., Apweiler, R., Aturaliya, R. N., Bailey, T. L., Bansal, M., Baxter, L., Beisel, K. W., Bersano, T., Bono, H., Chalk, A. M., Chiu, K. P., Choudhary, V., Christoffels, A., Clutterbuck, D. R.,

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The transcriptional landscape of the mammalian genome
Science 309 (5740), 1559-1563 (2005)
16141072

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COMMENT

FEATURES

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		putative"			
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		Best Local Similarity 80.5%; Pred. No. 0;			
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Qy	352	TGAAGAACCTGACACATCAGCATATATGTCAACTCTACCATGTGCTAGACAGCCAAACA	411		
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RESULT 5

AKI67457 2447 bp mRNA linear HTC 21-SEP-2005
Mus musculus 12 days pregnant adult female placenta cDNA, RIKEN
full-length enriched library, clone:1530014.15 product:maternal
embryonic leucine zipper kinase, full insert sequence.

ACCESSION

AKI67457

VERSION

AKI67457.1 GI:74195446

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

1

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

AUTHORS

10349636

TITLE

2

Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL

11042159

PUBMED

AUTHORS

3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Kono, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, W., Nishine, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., Kasukawa, T., Saito, R., RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 11076861
 4
 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, P., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsch, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wyehaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohatsu, S., and Hayashizaki, Y.
 RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
 Functional annotation of a full-length mouse cDNA collection
 Nature 409 (6821), 685-690 (2001)
 11217851
 5
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Brad, D., Brusa, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.P., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierzki, R.M., King, B.L., Konagawa, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reid, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempole, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kigawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
 FANTOM Consortium
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420 (6915), 563-573 (2002)
 12466851
 6
 Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E., Ambesi-Impombato, A., Apweiler, R., Aturaliya, R.N., Bailey, T.L., Bansal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R.,

Crowe, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagioli, M., Farkner, G., Fletcher, C.P., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingras, T.R., Gojobori, T., Green, R.E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Humnietek, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kelsso, J., Kitamura, H., Kitano, H., Kollias, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.P., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan, Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, P., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakauchi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavese, J., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Sempole, C.A., Sano, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, S., Sugita, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamanishi, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Brusa, V., Quackenbush, J., Wahlstedt, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watahiki, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.
 FANTOM Consortium
 The transcriptional landscape of the mammalian genome
 Science 309 (5740), 1559-1563 (2005)
 16141072
 7
 Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yagi, K., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sandelin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlstedt, C.
 RIKEN Genome Exploration Research Group
 Antisense transcription in the mammalian transcriptome
 Science 309 (5740), 1564-1566 (2005)
 16141073
 8 (bases 1 to 2447)
 Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/
 Location/Qualifiers
 1. .2447
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		Matches 1905; Conservative			
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Qy	172	TGAAGATTATGATGAACCTCTCAAAATATAT	TATGAATTACATGAAACTAT	TTGGGACAGGTG	231
Db	120	TGAAGATTATGACGAACCTCCTCAAAATAC	TATGAATACTATATGAACAGAT	TTGGGACAGGTG	179
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Qy	712	AAGCAATATCATATCTTTGGATTC	AGAGGACAGATTTTGGACATG	GGGCATATCTGTTATATG	771
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1. .2489

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/db_xref="taxon:10090"

/clone="C530047P13"

/issue_type="spinal cord"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="12 days embryo"

162_2093

/note="unnamed protein product; maternal embryonic leucine zipper kinase (MGL|GI:106924 GB|NM_010790, evidence: BLASTN, 99%, match=2489)

putative"

/codon_start=1

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Query Match

Best Local Similarity

Matches 1905; Conservative 0; Mismatches 422; Indels 40; Gaps 7

62.4%; Score 1541.8; DB 6; Length 2489;

80.5%; Pred. No. 0;

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171

DB

103

GCTGGGCCCGCTGCCCTCAGGTTCTGGTTGTCATTTTCAATAACCTTCAGGTGACTA

162

QY

172

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231

DB

163

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232

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DB

223

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711

DB

643

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702

Ambsi-Impionbato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dallymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.P., Fukushima,T., Furuno,M., Putaki,S., Gariboldi,M., Georgii-Hemming,P., Gingers,T.R., Gojohori,T., Green,R.E., Gustinchin,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hall,D., Huminicki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelsa,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L.L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakachi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Ohara,O., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.P., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiyura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichman,S.A., Ueda,H.R., van Nimwegen,B., Verardo,R., Wei,C.L., Yeghi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hilde,W., But,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

FANTOM Consortium

The transcriptional landscape of the mammalian genome

Science 309 (5740), 1564-1566 (2005)

16141072

7

Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

RIKEN Genome Exploration Research Group

Antisense transcription in the mammalian transcriptome

Science 309 (5740), 1564-1566 (2005)

16141073

8

(bases 1 to 2489)

Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Inotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

Direct Submission

Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

Location/Qualifiers

CONSRMT

TITLE

JOURNAL

PUBLISHED

REFERENCE

AUTHORS

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QY	712	AAGGCAATCATATCTTTGGATCAGAGGCAGATGTTTCGAGCATAGGGCATACTGTTATATG	771
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DB	883	AGCAGATGTTGCAGGTGGACCCAAAGAAACGGATTTCTATGAGAAATCTCTCGAACCATC	942
QY	952	CCTGGATCATGCAAGATTACAACTATCCTGTTGATGGCAAGCAAGAAATCCTTTTATTC	1011
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DB	1003	ACCTCGATGAGGATTCGTGACAGAGCTTTCTGTATATCACCGACGACGAGCGAGCAAA	1062
QY	1072	TGGAGGATTTAATTTCACTTGGCAGTATGATCACTCAGCGGTACCTATCTTTCTGCTTC	1131
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DB	1291	TATTA-----GCTCCCAAGACGCCACAGGTTACCAACACTTGGCAGAAATCAA	1338
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DB	1339	ATCAGCGAGCATCTAAATCAACGCGCCAGGGTACGACAGCAGTGGCAATAAATAAATAA	1398
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QY	1612	AAATACCAAGTAAATTCACAGCAACAGCAAGATTTAATGACAGGTGTCTATAGCCCTGAGA	1671
DB	1579	GAAACACAGGAAATTCGACAGAGCGAGCACACTTAACGACAGGTGTCTATAGCCCCGAGA	1638
QY	1672	GGCGTGGCGCTCAGTGGAAATGGATCTCAACCAAGCACATATGGAGGAGATCTCCAAAAA	1731
DB	1639	GGAGGTGCGGTTCAATGAGACGTGGATCTCAACCAAGGCACATGGAGGATACCCCGAAAA	1698
QY	1732	GAAAGGAGCAAGATGTTTGGAGCCTTGAAGGGGGTGGATAAGGTTATCACTGTGC	1791
DB	1699	AGAAAGGAAACCAATGTGTTTGGAGCCTTTGAGAGAGGACTGGATAAGGTTCTCACTCGC	1758
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[illegible]


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Db 1801 TCACAAGGACAAAGAGAGGGCTCTGCCAGAGATGGACCAAGAAAGCGAAGCTGCACT 1860
QY 1852 ATAAATGTGACTACAACTAGATTAGTGAATTCAGATCACTGTTGTAATGAATGAATGCTTA 1911
Db 1861 ACAATGTGACTACAACTAGCTGCTGTTGAACCAACGACGCTCTGAGCGGAATCATGGCTA 1920
QY 1912 TTCTTCCAAAGAGCATGTTGACTTTGTACAAAAGGTTATACATCGAAGTGTCAAAACAC 1971
Db 1921 TTCTTCCAAAGAGCATGTTGACTTTGTACAAAAGGTTATACATCGAAGTGTCAAAACG 1980
QY 1972 AGTCAGATTTGGAAAGTGACAAATGCAATTTGAATTTAGAAGTGTCCAGCTTCAAAAC 2031
Db 1981 AGTCAGATTTGGAAAGTGACAAATGCAATTTGAATTTAGAAGTGTCCAGCTTCAAAAC 2040
QY 2032 CGATGTGTTGGTATCAGAGGACGCGCTTAAGGCGCATGCTGGGTTTACAAAGAT 2091
Db 2041 CTGACGTGTAGGATCCGAGACAGCGCTGAAGGGTGAAGCTTGAAGTGTCAAAAGC 2100
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Db 2101 TAGTGAAGATATCTTGTCTGCTGCAAGATGACCGATGACAGTGTCCGCTGCGCGG 2160
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Db 2221 ATTGGATCTATGGAATCACAATCTGTTCTTAAAGAGTATCTTAAAGACCAATATCTCTT 2278
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Db 2338 TCAATTAATCTCTGTTTAAATCATG-GGCTTGTGATGTTAGTAATG-----TTTTAT 2390
QY 2384 ATTCACTTCCATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 2443
Db 2391 ATTCACTTCCATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 2450
QY 2444 TTCTGAAATATAACCAATTTGTGAATAT 2470
Db 2451 TTCTGAACTAAACCAATTTGTGAATAT 2477

RESULT 8
BC020416
LOCUS BC020416.1 GI:18042795
DEFINITION Mus musculus maternal embryonic leucine zipper kinase, mRNA (cdna
clone IMAGE:3588164).
ACCESSION BC020416
VERSION BC020416.1
KEYWORDS Mus musculus
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2396)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altshul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, I., Wang, J., Hsieh, P.,
Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Udén, T.B., Toshiyuki, S.,
Carninci, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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CONSRMT
TITLE
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AUTHORS
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REMARK
COMMENT
Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2 (bases 1 to 2396)
NIH MGC Project
Direct Submission
Submitted (03-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louesged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK plate: 10 Row: b Column: 2
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6680605
This clone has the following problem: no 5' EST match.
Location/Qualifiers
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arose spontaneously from a senescent normal mammary
(clonal) outgrowth infected with the virus MMTV."
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/note="Vector: pCMV-SPORT6"
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FEATURES

source

ORIGIN

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Best Local Similarity 80.6%; Pred. No. 0;
Matches 1884; Conservative 0; Mismatches 412; Indels 41; Gaps 7;
QY 143 TAAATTCAAATAAACTTGCAGAGAGCATGTAAGAGATTATGATGAACCTTCTCAAAATATTA 202
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QY	2296	ATGAATCTAAATCAAGCCCATCTGTCAATPAT--GTACTGTCTTTTAAATCAATGTGGTT	2353
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QY	2414	AACATGCTCTCTTTGTAATGTGTAATTTCTTTCTGAAATAAAACCAATTTTGTGAATAT	2470
Db	2250	CAGTGTGACTCATTTTGTGATACAGTTTCTTTCTGAACTAAAAACCAATTTTGTGAATAT	2306

CONSRMT	RIKEN Genome Exploration Research Group	QY	472	AGGATCGCTGT	CAGAAGAGGAGAC	CCGGTGTCTT	CCGTGATAGTAT	CTGCTGTG	531
TITLE	Anticence transcripion in the mammalian transcriptome	Db	521	AGGATCGCTGT	CGGAAGAGGAGAC	CCGGTGTCTT	CCGTGATAGTAT	CTGCTGTG	580
JOURNAL	Science 309 (5740), 1564-1566 (2005)								
PUBMED	16141073								
REFERENCE	8 (bases 1 to 2559)	QY	532	CTTATGTGCA	CAGCCA-GGGCTAT	CTCAGAGGACCT	CAAGCCAGAAAAT	TTGCTGTT	590
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.	Db	581	CGTATGTCC	ACAGCCAGGGGCT	TATCCCACAGGACCT	CAAAACCAAGAAAAT	TTATATTT	640
	Direct Submission	QY	591	GATGAATAT	CAATAAATAAGCT	GATGACTTTGGT	CTGTGCAAAACCC	CAAGGGTAAC	650
	Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of	Db	641	GATGAATAAT	CTAAGCTAAAGCT	GATGACTTTGGT	CTGTGCAAAACCC	CAAGGGCAAC	700
TITLE	Physical and Chemical Research (RIKEN), Laboratory for Genome	QY	651	AAGGATTACC	ATCTACAGACAT	GTGTGGAGCT	TGGCTTATGCGAC	CTCAGATTAA	710
JOURNAL	Exploration Research Group, RIKEN Genomic Sciences Center (GSC),	Db	701	AAGGACTACC	ATCTCGACAGOG	TGTGTGGAGCCT	TGCTTATGCGAG	CTCTGAATTA	760
	RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,	QY	711	CAAGCAATCA	TATCTTGGATC	AGAGGAGATG	TTTGGAGATGG	GCATCTGTATAT	770
	Kanagawa, 230-0045, Japan (E-mail:genome-res@sc.riken.jp,	Db	761	CAAGGAAAT	CTGTACCTTGGAT	CAGAGGAGAT	TTTGGAGATGG	GCATCTGTAT	820
	URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,	QY	771	GTTCCTAT	GTGGATTCTTAC	CAATTTGATGAT	ATAATGTAAT	TGCTTTATAC	830
	Fax:81-45-503-9216)	Db	821	GTGCTCAT	GTGGATTCTTAC	CAATTTGATGAT	ATAATGTAAT	TGCTTTATAC	880
COMMENT	cDNA library was prepared and sequenced in Mouse Genome	QY	831	ATTATGAG	AGGAAAATATGAT	GTTCCTCAAG	TGGCTCTCT	CTCCAGTAG	890
	Encyclopedia Project of Genome Exploration Research Group in Riken	Db	881	ATAATGAG	AGGAAAATACGA	GTTCCTCAAG	TGGCTCTCT	CTCCAGTAG	940
	Genomic Sciences Center and Genome Science Laboratory in RIKEN.	QY	891	CAACAAAT	GTGCGTGGAC	CCCAAGAAAC	CGGATTTCTAT	GAAAATCTAT	950
	Division of Experimental Animal Research in Riken contributed to	Db	941	CAGCAGAT	TTTGCAGGTGG	ACCCAAAGAA	ACCGATTTCTAT	GAGAAATCT	1000
	prepare mouse tissues.	QY	951	CCCTGATCA	TGCAAGATTAC	AACTATCTGT	TGAGTGCA	AAAGCAAGAT	1010
	Please visit our web site for further details.	Db	1001	CCCTGGTCA	TGCAAGATTAC	AACTATCTGT	TGAGTGCA	AAAGCAAGAT	1060
FEATURES	URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/ Location/Qualifiers	QY	1011	CACCTCGAT	GTGATTTGGCTAA	CAGAACTTTCT	GTACATCAC	AGAAACCA	1070
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Matches 1906; Conservative	0; Mismatches 421; Indels 42; Gaps 9;	QY	1191	CAAGCCAG	TGTACCCCAAT	TCACAGACAT	CAAGTCA	AAATTAAT	1250
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QY 1298 GTGTGAAGATGATTTATCAACAGGTGTCTACTCTCCCGAAACATCACAGTTTACCAAGTA 1357
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QY 1418 TGCAAAATAAATTAAGAAACAAAGAAATGTATATCTCTTAAGTCTGCTGTTAAAGAAATGA 1477
Db 258 TGCAAAATAAATTAAGAAACAAAGAAATGTATATCTCTTAAGTCTGCTGTTAAAGAAATGA 199
QY 1478 AGAGTACTTATGTTTCTGAGCCAAAGACTCCAGTTTAAAGAAACCAAGCAATGAAGAGA 1537
Db 198 AGAGTACTTATGTTTCTGAGCCAAAGACTCCAGTTTAAAGAAACCAAGCAATGAAGAGA 139
QY 1538 ATACTACTACCTACCCAAATGGTTTACTACTACACACCTCAAAAGCTAGAAACAGTGCCTGAA 1597
Db 138 ATACTACTACCTACCCAAATGGTTTACTACTACACACCTCAAAAGCTAGAAACAGTGCCTGAA 79
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AL554470 1030 bp mRNA linear EST 30-MAR-2004
LOCUS AL554470 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1084Y107 5-PRIME, mRNA sequence.
ACCESSION AL554470
VERSION AL554470.3 GI:45859224
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1030)
Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31276280.
Contact: Genoscope
```

Genoscope - Centre National de Sequencage
2 rue Gaston Cremlieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5403.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1084Y107&p1sc=5403.f.

FEATURES

source

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ORIGIN

Query Match 41.3%; Score 1020.6; DB 1; Length 1030;
Best Local Similarity 99.5%; Pred. No. 3.9e-253;
Matches 1020; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY 901 TGCAGGTGGACCCCAAGAAACCGATTCTATGAAAAATCTATTGAACCATCCCTGGATCA 960
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DEFINITION AGENCOURT_6727232 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:5798927
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VERSION BM928784.1 GI:19379173
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1091)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-k@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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High quality sequence stop: 708.
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FEATURES
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II RT (Life Technologies). Note: this is a NIH_MGC Library."

Query Match 35.3%; Score 872.4; DB 3; Length 1091;
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Matches 913; Conservative 0; Mismatches 12; Indels 4; Gaps 3;

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QY 1019 TGATGATTCGCTAAACAGAACTTTCTGTACATCACAGAAACCAAGCAACCAATGGAGGA 1078
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QY 1079 TTTAAATTTCACTGTGGCAGTATGATCACCTCACGGCTACCTATCTTCTGCTTCTAGCCAA 1138
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QY 1139 GAAGGCTCGGGGAAACCCAGTTCTGTTTAAAGGCTTTCTTCTCTCTGCGAAGCCAG 1198
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QY 1199 TGTACCCCATTTCAAGATCAAGTCAATTAATGGAAGTCTGGAAGATGTGACCCCAAG 1258
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QY 1439 AGAAATGTATATACTCTCTAAAGTCTGCTGTAAGATGAAGAGTACTTTATGTTTCTCTGA 1498
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QY 1499 GCCAAAGACTCCAGTTTAAGAACCCAGCATTAAGAGAGAAATCTCACTACGCCAAATCG 1558
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QY 1559 TTACACTACACCTCAAAAGCTAGAACCCAGTCCCTGGAAGAACTCCCAATTAATAATACC 1618
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QY 1619 AGTAAATTCACAGGAACAGACAAGTTAATGACAGGTGTCAATTAGCCCTGAGAGCGGTG 1678
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VERSION
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  Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
  Hubisz, M.J., Fiedel-Alon, A., Tanenbaum, D.M., Civallo, D.,
  White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
  A Scan for Positively Selected Genes in the Genomes of Humans and
  Chimpanzees
  (er) PLoS Biol. 3 (6), E170 (2005)
  15869325
  2 (bases 1 to 1898)
  Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
  Hubisz, M.J., Fiedel-Alon, A., Tanenbaum, D.M., Civallo, D.,
  White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
  Direct Submission
  Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
  Rockville, MD 20850, USA
  This sequence was made by sequencing genomic exons and ordering
  them based on alignment. Translation starts at the beginning of
  alignment.
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	2470	100.0	2470	7	US-10-354-358-7
5	2470	100.0	2470	7	US-10-172-118-1535
6	2470	100.0	2470	7	US-10-295-027-505
7	2470	100.0	2470	7	US-10-173-999-126
8	2470	100.0	2470	8	US-10-342-887-1535
9	2470	100.0	2470	9	US-10-656-598-1
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11	2470	100.0	2470	10	US-10-848-755A-169
12	2470	100.0	2470	10	US-10-843-641A-4148
13	2470	100.0	2470	10	US-10-756-149-2259
14	2470	100.0	2470	10	US-10-770-726-23
15	2470	100.0	2470	12	US-10-960-414-132
16	2470	100.0	2470	15	US-11-177-138-9
17	2470	100.0	2487	8	US-10-425-114-26285

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19	2452	99.3	2463	8	US-10-425-114-26959	Sequence 26959, A
20	2441	98.8	2441	8	US-10-425-114-26835	Sequence 26835, A
21	2438	98.7	2453	3	US-09-974-298-111	Sequence 111, App
22	2438	98.7	2501	10	US-10-955-054A-138	Sequence 138, App
23	2159.8	87.4	2519	6	US-10-071-766-82	Sequence 82, Appl
24	2127.6	86.1	2162	3	US-09-822-849A-483	Sequence 483, App
25	1398.4	56.6	1400	13	US-11-060-756-1002	Sequence 1002, Ap
26	1398.4	56.6	1400	13	US-11-060-756-5274	Sequence 5274, Ap
27	855.4	34.6	877	3	US-09-764-875-308	Sequence 308, App
28	843.2	34.1	887	6	US-10-106-698-1036	Sequence 1036, Ap
29	720.8	29.2	1673	3	US-09-814-353-21017	Sequence 21017, A
30	524	21.2	15985	15	US-11-121-086-56	Sequence 56, Appl
31	512	20.7	512	6	US-10-656-598-13	Sequence 13, Appl
32	507.6	20.6	606	6	US-10-106-698-2000	Sequence 2000, Ap
33	437.8	17.7	489	3	US-09-764-868-222	Sequence 222, App
34	437.8	17.7	489	3	US-09-764-875-585	Sequence 585, App
35	410	16.6	410	9	US-10-696-639-1095	Sequence 1095, Ap
36	385.8	15.6	423	3	US-09-918-995-33354	Sequence 33354, A
37	373	15.1	373	3	US-09-822-830A-155	Sequence 155, App
38	268.8	10.9	499	3	US-09-783-590-8126	Sequence 8126, Ap
39	256	10.4	496	3	US-09-783-590-7891	Sequence 7891, Ap
40	228	9.2	572	3	US-09-864-761-13539	Sequence 13539, A
41	228	9.2	572	13	US-11-060-756-1430	Sequence 1430, Ap
42	228	9.2	572	13	US-11-060-756-1431	Sequence 1431, Ap
43	228	9.2	572	13	US-11-060-756-5702	Sequence 5702, Ap
44	228	9.2	572	13	US-11-060-756-5703	Sequence 5703, Ap
45	208.4	8.4	1863	9	US-10-635-398-109	Sequence 109, App

ALIGNMENTS

RESULT 1
US-09-870-937-9
; Sequence 9, Application US/09870937
; Patent No. US20020049180A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Bin
; APPLICANT: Seeley, Todd
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEOPLASTIC DISEASE USING
; FILE REFERENCE: CHEMOTHERAPY AND RADIATION SENSITIZERS
; FILE REFERENCE: 200130.514/PP-01623.002
; CURRENT APPLICATION NUMBER: US/09/870,937
; CURRENT FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2470
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-870-937-9

Query Match 100.0%; Score 2470; DB 3; Length 2470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TTGGCGGGCGGAGCGGCACACACCGCGGATCGAAAGATTCTTAGAACCGCGTACCA	60
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Qy	61	GC CGCGTCTCTCAGGACAGCAGCGCCCTCTCTCTCTGTCGGCGCGCTCAGCGTGC	120
Db	61	GC CGCGTCTCTCAGGACAGCAGCGCCCTCTCTCTCTGTCGGCGCGCTCAGCGTGC	120
Qy	121	TCCGCCCTCAGGTTCTTTTCTAATTCAAATAAACTTGAAGAGGACTTGAAGATT	180
Db	121	TCCGCCCTCAGGTTCTTTTCTAATTCAAATAAACTTGAAGAGGACTTGAAGATT	180
Qy	181	ATGATGAACCTTCAATATTTATGATTAACATGAACCTTGGGACAGTGGCTTGC	240
Db	181	ATGATGAACCTTCAATATTTATGATTAACATGAACCTTGGGACAGTGGCTTGC	240

Qy	241	AGGTCAAACTTGGCTGCCATATCTTTACTCGAGAGATGGTAGCTATAAAAAATCATGGATA	300
Db	241	AGGTCAAACTTGGCTGCCATATCTTTACTCGAGAGATGGTAGCTATAAAAAATCATGGATA	300
Qy	301	AAAACACACTAGGGAGTGATTTGCCCGGATCAAAACGGAGATTTGAGGCTTCAAGAACC	360
Db	301	AAAACACACTAGGGAGTGATTTGCCCGGATCAAAACGGAGATTTGAGGCTTCAAGAACC	360
Qy	361	TGAGACATCAGCATATATGTCAACTTCACCATGTGCTAGAGACAGCCAAACAAAATATTCA	420
Db	361	TGAGACATCAGCATATATGTCAACTTCACCATGTGCTAGAGACAGCCAAACAAAATATTCA	420
Qy	421	TGGTTCCTTGAGTACTGCCCTTGAGGAGAGCTGTTGACTATATAATTTCCAGGATCGCC	480
Db	421	TGGTTCCTTGAGTACTGCCCTTGAGGAGAGCTGTTGACTATATAATTTCCAGGATCGCC	480
Qy	481	TGTCAGAAAGGAGAGACCCGGGTTGTCTTCGTGACAGATAGTATCTGCTGTTGCTTATGTGC	540
Db	481	TGTCAGAAAGGAGAGACCCGGGTTGTCTTCGTGACAGATAGTATCTGCTGTTGCTTATGTGC	540
Qy	541	ACAGCCAGGCTATGTCTCA CAGGGA CCTCAAGCCAGAAAAATTTGCTGTTTGATGAATATC	600
Db	541	ACAGCCAGGCTATGTCTCA CAGGGA CCTCAAGCCAGAAAAATTTGCTGTTTGATGAATATC	600
Qy	601	ATAAAATTAAGCTGATTTGACTTTTGCTCTCTGTCGCAAAACCAAGGTTAAACAAGATTACC	660
Db	601	ATAAAATTAAGCTGATTTGACTTTTGCTCTCTGTCGCAAAACCAAGGTTAAACAAGATTACC	660
Qy	661	ATCTACAGACATGCTGTGGGAGTCTGGCTTATG CAGCACCTGAGTTTAATAACAAGGCAAAAT	720
Db	661	ATCTACAGACATGCTGTGGGAGTCTGGCTTATG CAGCACCTGAGTTTAATAACAAGGCAAAAT	720
Qy	721	CATATCTTGGATCAGAGGCAGATGTTTGGAGCATGCGGCATCTGTTTATATGTTCTTATGT	780
Db	721	CATATCTTGGATCAGAGGCAGATGTTTGGAGCATGCGGCATCTGTTTATATGTTCTTATGT	780
Qy	781	GTGGATTTCTACCAATTTGATGATGAATAATGTAA TGGCTTTATACAAGACATTTATGAGAG	840
Db	781	GTGGATTTCTACCAATTTGATGATGAATAATGTAA TGGCTTTATACAAGACATTTATGAGAG	840
Qy	841	GAAATATGATGTTTCCCAAGTGGCTCTCTCCAGTAGCATTTCTGTTCTTTCACAAATGC	900
Db	841	GAAATATGATGTTTCCCAAGTGGCTCTCTCCAGTAGCATTTCTGTTCTTTCACAAATGC	900
Qy	901	TGCAGGTGGACCCAAAGAAAGGATTTCTATGAAAAATCTATTGACACCATCCCTGGATCA	960
Db	901	TGCAGGTGGACCCAAAGAAAGGATTTCTATGAAAAATCTATTGACACCATCCCTGGATCA	960
Qy	961	TGCAAGATTACAACTATCTCTGTGAGTGGCAAGAAAGATTCCTTTTATTCACCTCGATG	1020
Db	961	TGCAAGATTACAACTATCTCTGTGAGTGGCAAGAAAGATTCCTTTTATTCACCTCGATG	1020
Qy	1021	ATGATTCGGTAA CAGAACTTTCTGTATCATACAGAAA CAACAGGCACCAATCGAGGATT	1080
Db	1021	ATGATTCGGTAA CAGAACTTTCTGTATCATACAGAAA CAACAGGCACCAATCGAGGATT	1080
Qy	1081	TAAATTTCACTGTGGCAGTATGATCACTCAGGCTACCTATCTTCTGTTCTAGGCCAAGA	1140
Db	1081	TAAATTTCACTGTGGCAGTATGATCACTCAGGCTACCTATCTTCTGTTCTAGGCCAAGA	1140
Qy	1141	AGGCTCGGGGAAAA CCAAGTTCTGTTTAAAGGCTTTCTTTTCTCCTGTGGACAAGCCAGTG	1200
Db	1141	AGGCTCGGGGAAAA CCAAGTTCTGTTTAAAGGCTTTCTTTTCTCCTGTGGACAAGCCAGTG	1200
Qy	1201	CTACCCCAATTCACAGACATCAAGTCAAAATTAATTTGGAGTCTGGAGATGTCACCGCAGTG	1260
Db	1201	CTACCCCAATTCACAGACATCAAGTCAAAATTAATTTGGAGTCTGGAGATGTCACCGCAGTG	1260
Qy	1261	ATAAAAAATTAATGTGGCGGGATTAATAGACTATGATCTATGATTTGGTGTGAAGATGATTTATCAACAG	1320
Db	1261	ATAAAAAATTAATGTGGCGGGATTAATAGACTATGATCTATGATTTGGTGTGAAGATGATTTATCAACAG	1320

Qy	1321	GTGCTGCTACTCCCCGNAATCA	CAGTTTTACCAAGTACTGGACAGAA	TCAAAATGGGGTGG	1380	
Db	1321	GTGCTGCTACTCCCCGNAATCA	CAGTTTTACCAAGTACTGGACAGAA	TCAAAATGGGGTGG	1380	
Qy	1381	AACTAAATCA	TAACTCCAGCCTTATGCAGAA	CACCTGCAAAATAAATAAAGAACAAAG	1440	
Db	1381	AACTAAATCA	TAACTCCAGCCTTATGCAGAA	CACCTGCAAAATAAATAAAGAACAAAG	1440	
Qy	1441	AAAATGTA	TATACCTCCTTAAGTCTGTGAAGAATGAAGTA	CTTTTATGTTTCTTGAGC	1500	
Db	1441	AAAATGTA	TATACCTCCTTAAGTCTGTGAAGAATGAAGTA	CTTTTATGTTTCTTGAGC	1500	
Qy	1501	CAAGACTCCAG	TTTTAATGAACACGACATAAAGAGAGAA	TACTCCTACGCCAAATCGTT	1560	
Db	1501	CAAGACTCCAG	TTTTAATGAACACGACATAAAGAGAGAA	TACTCCTACGCCAAATCGTT	1560	
Qy	1561	ACACTACAC	CCCTCAAAGCTAGAAACACAGTGCCTGAAAGAAAT	TCCAAATTAATAATACCCAG	1620	
Db	1561	ACACTACAC	CCCTCAAAGCTAGAAACACAGTGCCTGAAAGAAAT	TCCAAATTAATAATACCCAG	1620	
Qy	1621	TAAATTC	CAAGNACAGACAAAGTTAATGACAGGTGTCA	TTAGCCCTGAGAGCGGTGCC	1680	
Db	1621	TAAATTC	CAAGNACAGACAAAGTTAATGACAGGTGTCA	TTAGCCCTGAGAGCGGTGCC	1680	
Qy	1681	GCTCAGTGG	AAATGGATCTCAACCAACGACATATGGAGGAGACT	TCCAAAAGAAAGAGGGAG	1740	
Db	1681	GCTCAGTGG	AAATGGATCTCAACCAACGACATATGGAGGAGACT	TCCAAAAGAAAGAGGGAG	1740	
Qy	1741	CCAAAGG	TTTTGGAGCCTTGAAAGGGGTTGGATTAAG	AGTTTACATGTGCTCACACAGGA	1800	
Db	1741	CCAAAGG	TTTTGGAGCCTTGAAAGGGGTTGGATTAAG	AGTTTACATGTGCTCACACAGGA	1800	
Qy	1801	GC	AAAAGGAAGGTTCTGC	CAGAGACGGGCCCAGAGACTTAAAGCTT	TCACTATAATGTGA	1860
Db	1801	GC	AAAAGGAAGGTTCTGC	CAGAGACGGGCCCAGAGACTTAAAGCTT	TCACTATAATGTGA	1860
Qy	1861	CTACAA	CTAGATAGTGAATCCAGATCAA	CTGTTTGAATGAATAATGTCTATTTCTTCCAA	1920	
Db	1861	CTACAA	CTAGATAGTGAATCCAGATCAA	CTGTTTGAATGAATAATGTCTATTTCTTCCAA	1920	
Qy	1921	AGAAGCA	TGTTGACTTTGTA	CAAAAGGGTTATACATCTGAAGTGTCAAAACACAGTCAGATT	1980	
Db	1921	AGAAGCA	TGTTGACTTTGTA	CAAAAGGGTTATACATCTGAAGTGTCAAAACACAGTCAGATT	1980	
Qy	1981	TTGG	AAAGTGACAATCAATTTTGAATAGAGTGTGCCAGCTT	CABAAAACCCGATGTGG	2040	
Db	1981	TTGG	AAAGTGACAATCAATTTTGAATAGAGTGTGCCAGCTT	CABAAAACCCGATGTGG	2040	
Qy	2041	TGGGTAT	CAGAGGACGGCCTTAAGGGCGATGCTGGGTTT	TACAAAAGATTAAGTGGAA	2100	
Db	2041	TGGGTAT	CAGAGGACGGCCTTAAGGGCGATGCTGGGTTT	TACAAAAGATTAAGTGGAA	2100	
Qy	2101	ACAT	CTTACTAGCTGCAAGGTATAATGATGGAATCTTCCATCTG	CCGGATGAGTGTG	2160	
Db	2101	ACAT	CTTACTAGCTGCAAGGTATAATGATGGAATCTTCCATCTG	CCGGATGAGTGTG	2160	
Qy	2161	GGTGTGA	TACAGCCTACATAAAGACTGTTATGATCGCTTTGATTT	TAAAGTTCAATGGAA	2220	
Db	2161	GGTGTGA	TACAGCCTACATAAAGACTGTTATGATCGCTTTGATTT	TAAAGTTCAATGGAA	2220	
Qy	2221	CTACCA	ACTTTGTTCTAAGAGCTATCTTAAGACCAATATCTCTTTG	TTTTTAAACAAA	2280	
Db	2221	CTACCA	ACTTTGTTCTAAGAGCTATCTTAAGACCAATATCTCTTTG	TTTTTAAACAAA	2280	
Qy	2281	GATATTA	TTTTTGATGAATCTAAATCAAGCCCATCTGT	CATTATGTTACTGTCTTTTT	2340	
Db	2281	GATATTA	TTTTTGATGAATCTAAATCAAGCCCATCTGT	CATTATGTTACTGTCTTTTT	2340	
Qy	2341	TAA	TCATGCGTTTGTATTAATAAATATGTTGACTTTT	CTTAGATTCACCTCCATATGTG	2400	
Db	2341	TAA	TCATGCGTTTGTATTAATAAATATGTTGACTTTT	CTTAGATTCACCTCCATATGTG	2400	
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Db 2401 AATGTAAGCTCTTAACATATGCTCTTTGTAATGTGTAATTTCTTCTGAAATAAACCAT 2460
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RESULT 2
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; Sequence 1121, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
; FILE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1121
; LENGTH: 2470
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1121

Query Match 100.0%; Score 2470; DB 3; Length 2470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGCGGCGGAAGCGGCCACCAACCGCGGATCGAAAGATTCTTAGGAACGCGGTACCA 60
Db 1 TTGGCGGCGGAAGCGGCCACCAACCGCGGATCGAAAGATTCTTAGGAACGCGGTACCA 60

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Qy 121 TCGGCCCTCAGGTCTTTTCTAATTCGAATAAATCTTGAAGAGGACTATGAAGATT 180
Db 121 TCGGCCCTCAGGTCTTTTCTAATTCGAATAAATCTTGAAGAGGACTATGAAGATT 180

Qy 181 ATGATGAATCTCTCAATATATTAATACATGAATCTTGGGACAGGTGCTTTGCCA 240
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Qy 241 AGGTCAAACTTGCCTGCCATATCTTCTACTGAGAGATGTTAGCTATAAAATCATGGATA 300
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Qy 301 AAAACACACTAGGAGTGTATTTGCCCGGATCAAAACCGAGATTGAGGCTTTGAAGAAC 360
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Db 421 TGGTTCTTGAGTACTGCCCTGGAGGAGAGCTGTTTGACTATATATAATTTCCAGGATCGCC 480
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Db 541 ACAGCAGCGGCTATGCTCAAGGGACCTCAAGCCAGAGAAAATTTGCTTTGATGAATATC 600
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Qy 661 ATCTACAGACATGCTGTGGGAGTCTGGCTTATGCAGCACCTGAGTTAATACAAAGCAAT 720
Db 661 ATCTACAGACATGCTGTGGGAGTCTGGCTTATGCAGCACCTGAGTTAATACAAAGCAAT 720
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Db 721 CATATCTTTGGATCAGAGGACAGATGTTGGAGCATGGCATACTGTTATATGTTCTTATGT 780
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Qy 841 GAAATATGATGTTCCCAAGTGGCTCTCTCCAGTAGCATTTCTGCTTCTTCAACAAATGC 900
Db 841 GAAATATGATGTTCCCAAGTGGCTCTCTCCAGTAGCATTTCTGCTTCTTCAACAAATGC 900
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Db 1081 TAAATTTCACTGTGGCAGTATGATCACTCAGGGTACCTATCTCTGCTTCTAGCAAGA 1140
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Db 1141 AGGCTCGGGGAAACCAAGTTGTTTAAAGCTTTCTTCTTCTCTGCTGTGCAAGCAGTG 1200
Qy 1201 CTACCCCAATTCAGACATCAAGTCAATTAATGAGTCTGGAAGATGTCGCGCAAGTG 1260
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Db 1261 ATAAATTAATGTCGCGGATTAATAGACTATGATTTGGTGTGAAGATGATTATCAACAG 1320
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1561 ACACATACACCTCAAAAGCTAGAAACAGCTGCTGAAAGAACTCCAAATTAATATACAG 1620
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1621 TAAATTAACAGAGAACAGACAGTAAATGACAGGTGTCAATAGCCCTGAGAGCGGTGCC 1680
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1861 CTACAACTAGATTTAGTGAATCCAGATCAACTGTGTGAATGAATTAATGTCTATTTCCAA 1920
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2341 TAATCATGTGTTTTGTTATATTAATTAATGTTGACCTTTCTTAGATTTCACTTCCATATGTG 2400
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2401 AATGTAAGCTCTTAACTATGCTCTTTGTAATGTTAAATTTCTTCTGAAATAAACCAT 2460
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RESULT 3
US-09-880-107-1725
; Sequence 1725, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1725
; LENGTH: 2470
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 D79997
US-09-880-107-1725

Query Match 100.0%; Score 2470; DB 3; Length 2470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TTGGCGGGCGGAAGCGGCCACAAACCGCGCATCGAAAGAGATCTTAGGAACCGCGTACCA 60
QY 61 GCCGCGTCTCTCAGACAGCAGCGCCCTGTCTTCTGTGGCGCGCGCTCAGCGGTGCC 120
DB 61 GCCGCGTCTCTCAGACAGCAGCGCCCTGTCTTCTGTGGCGCGCGCTCAGCGGTGCC 120
QY 121 TCCGCGCCCTCAGGTTCTTTTCTTAATTCNAATTAACCTTGCAGAGGACTATGAAGATT 180
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DB 181 ATGATGAACCTTCTCAAAATATTATGAATACATGAATATTTGGGACAGGTGCTTTGCAA 240
QY 241 AGGTCAAACTTGCCTGCCATATCTTACTGGAGAGATGGTAGCTATAAAATCATGGATA 300
DB 241 AGGTCAAACTTGCCTGCCATATCTTACTGGAGAGATGGTAGCTATAAAATCATGGATA 300
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QY 361 TCAGACATCAGCATATATGTCAACTCTACCATGTCTAGAGACAGCAACAAATATTCA 420
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QY 421 TGGTTCTTGAGTACTGCCCTGGAGGAGCTGTTTGACTATATAATTTCCAGGATCGCC 480
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[illegible]

Db	1681	GCTCAGTGGAAATTGGATCTCAACAAGCACAATATGGAGGAGATCTCAAAAAGAAAGGGAG	1740
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Db	1741	CCAAAGTGTTTGGGAGCCTTTGAAAGGGGGTTGGATAAGGTTATCACTGTGCTCACACAGGA	1800
Qy	1801	GCAAAAAGAAAGGGTTTGCACAGAGAGCGGCCCAAGAGACTTAAAGCTTCACTAATAATGTGA	1860
Db	1801	GCAAAAAGAAAGGGTTTGCACAGAGAGCGGCCCAAGAGACTTAAAGCTTCACTAATAATGTGA	1860
Qy	1861	CTACAACATAGATTAGTGAATCCAGATCAACTGTGTGAATGAAATAATGTCTATTTCTTCCAA	1920
Db	1861	CTACAACATAGATTAGTGAATCCAGATCAACTGTGTGAATGAAATAATGTCTATTTCTTCCAA	1920
Qy	1921	AGAGCATGTGTACTTTGTACAAAAGGGTTATACACTGAAGTGTCAAAACACAGTCAAGATT	1980
Db	1921	AGAGCATGTGTACTTTGTACAAAAGGGTTATACACTGAAGTGTCAAAACACAGTCAAGATT	1980
Qy	1981	TTGGGAAAGTGACAATCAATTTGAATTAGAAGTGTGCCAGCTTTCAAAAACCCGATGTGG	2040
Db	1981	TTGGGAAAGTGACAATCAATTTGAATTAGAAGTGTGCCAGCTTTCAAAAACCCGATGTGG	2040
Qy	2041	TGGGTATCAGGAGGACGGCTTTAAGGGCGATGCCTGGGTTTACAAAAGATTAGTGGAAAG	2100
Db	2041	TGGGTATCAGGAGGACGGCTTTAAGGGCGATGCCTGGGTTTACAAAAGATTAGTGGAAAG	2100
Qy	2101	ACATCTCTATCTAGCTGCAAGGTATAATTGATGATTCTTCCATCTCTCGGAGTGAAGTGTG	2160
Db	2101	ACATCTCTATCTAGCTGCAAGGTATAATTGATGATTCTTCCATCTCTCGGAGTGAAGTGTG	2160
Qy	2161	GGTGTGATACAGCCTACATAAAGACTGTTATGATCGCTTTGATTTTAAAGTTCATTGGAA	2220
Db	2161	GGTGTGATACAGCCTACATAAAGACTGTTATGATCGCTTTGATTTTAAAGTTCATTGGAA	2220
Qy	2221	CTACCAACTGTGTTCTTAAAGAGCTACTTAAAGACCAATATCTCTTTGTTTTTAAACAAA	2280
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Qy	2281	GATATTATTTTGTGTATGAATCTTAAATCAAGCCCATCTGTCAATTATGTTACTGTCTTTTT	2340
Db	2281	GATATTATTTTGTGTATGAATCTTAAATCAAGCCCATCTGTCAATTATGTTACTGTCTTTTT	2340
Qy	2341	TAATCATGTGGTTTTGTATATTAATAAATTTGTGACTTCTTAGATTCACTTCCATATGTG	2400
Db	2341	TAATCATGTGGTTTTGTATATTAATAAATTTGTGACTTCTTAGATTCACTTCCATATGTG	2400
Qy	2401	AATGTAAGCTCTTAACTATGTCTCTTTTGTAAATGTGTAAATTTCTTCTGAAATAAAACCAT	2460
Db	2401	AATGTAAGCTCTTAACTATGTCTCTTTTGTAAATGTGTAAATTTCTTCTGAAATAAAACCAT	2460
Qy	2461	TTGTGATAT	2470
Db	2461	TTGTGATAT	2470

RESULT 4
US-10-354-358-7
; Sequence 7, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Lesoon, Andrea
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; 7181, 7660, 2541, 69583, 49863, 8897, 1682, 17667, 9235,
; 7031, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
; 9252, 9389, 1642, 85369, 10297, 1594, 9525, 14124, 4469,

;/ TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
;/ TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
;/ TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
;/ FILE REFERENCE: MPI02-020PIRNONIM
;/ CURRENT APPLICATION NUMBER: US/10/354,358
;/ CURRENT FILING DATE: 2003-01-30
;/ PRIOR APPLICATION NUMBER: US 60/353,600
;/ PRIOR FILING DATE: 2002-01-31
;/ PRIOR APPLICATION NUMBER: US 60/364,517
;/ PRIOR FILING DATE: 2002-03-15
;/ PRIOR APPLICATION NUMBER: US 60/371,075
;/ PRIOR FILING DATE: 2002-04-09
;/ PRIOR APPLICATION NUMBER: US 60/371,507
;/ PRIOR FILING DATE: 2002-04-10
;/ PRIOR APPLICATION NUMBER: US 60/372,984
;/ PRIOR FILING DATE: 2002-04-16
;/ PRIOR APPLICATION NUMBER: US 60/374,194
;/ PRIOR FILING DATE: 2002-04-19
;/ PRIOR APPLICATION NUMBER: US 60/382,995
;/ PRIOR FILING DATE: 2002-05-24
;/ PRIOR APPLICATION NUMBER: US 60/385,023
;/ PRIOR FILING DATE: 2002-05-31
;/ PRIOR APPLICATION NUMBER: US 60/388,853
;/ PRIOR FILING DATE: 2002-06-14
;/ PRIOR APPLICATION NUMBER: US 60/389,395
;/ PRIOR FILING DATE: 2002-06-17
;/ Remaining Prior Application data removed - See File Wrapper or PALM.
;/ NUMBER OF SEQ ID NOS: 122
;/ SOFTWARE: FastSeq for Windows Version 4.0
;/ SEQ ID NO 7
;/ LENGTH: 2470
;/ TYPE: DNA
;/ ORGANISM: Homo sapiens
;/ FEATURE:
;/ NAME/KEY: CDS
;/ LOCATION: (171)...(2126)
;/ US-10-354-358-7

Query Match 100.0%; Score 2470; DB 7; Length 2470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 GCCGCGTCTCTCAGACAGAGCGCCCTGTCCTTCTGTGCGGCGCGCTCAGCCGTGCC 120
QY 121 TCCGCCCTCAGGTTCCTTTTCTTAATTCCAAATAAACTTGCAGAGAGACTATCAAGAATT 180
DB 121 TCCGCCCTCAGGTTCCTTTTCTTAATTCCAAATAAACTTGCAGAGAGACTATCAAGAATT 180
QY 181 ATGATGAACCTTCTCAATAATTATGAATATACATGAACACTATGGACAGGTGGCTTTCGAA 240
DB 181 ATGATGAACCTTCTCAATAATTATGAATATACATGAACACTATGGACAGGTGGCTTTCGAA 240
QY 241 AGGTCAAACTTGGCTGCTATCCTTACTGAGAGATGGTAGCTATAAAATCATGGATA 300
DB 241 AGGTCAAACTTGGCTGCTATCCTTACTGAGAGATGGTAGCTATAAAATCATGGATA 300
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DB 361 TGAGACATCAGCATATATGTCAACTCTACCTACCTATGCTGTAGACAGCCCAAAATATTC 420
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DB 421 TGGTCTTGTAGTACTGCCCTGGAGAGAGCTGTTTGACTATATAATTTCCAGGATCGCC 480

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DB 481 TGTCAAGAGAGAGACCCCGGGTGTCTTCCGTGATAGTATCTGCTGTGCTTATGTGC 540
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DB 541 ACAGCCAGGGCTATGCTCAGAGGACCTCAAGCCAGAAAATTTGCTGTTGATGATATC 600
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DB 661 ATCTACAGACATGCTGTGGGAGTCTGGCTTATGACGACCTGAGTTAATACAAAGCAAT 720
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DB 721 CATATCTTGGATCAGAGGAGATGTTTGGAGATGGGATCTGTTATATGTTCTTATGT 780
QY 781 GTGGATTTCTACATTTGATGATGATTAATGTAATGGCTTATACAAAGAGATTATGAGAG 840
DB 781 GTGGATTTCTACATTTGATGATGATTAATGTAATGGCTTATACAAAGAGATTATGAGAG 840
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DB 841 GAAAAATATGATGTTCCCAAGTGGCTCTCTCCAGTAGCATCTGCTTCTTCAACAAATGC 900
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DB 961 TGCAGGATTACAACTATCTCTGTGAGTGGCAAGCAAGAAATCTTTTATTTACCTCGATG 1020
QY 1021 ATGATTGGCGTAAACAGAACTTTCTGTACATCAGAGAAACAAACAGGCAAAATGGAGATT 1080
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DB 1201 CTACCCCATTTCAACAGATCAAGTCAAAATTAATTTGGAGTCTGGAAGATGTGACCGCAAGTG 1260
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QY 1381 AATCTAAATCATTAATCCAGCTTTATGAGAACACCTGCAAAATAAATTTAAAGAACAAAG 1440
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QY 1501 CAAAGACTCCAGTTAATAGAACACAGCATAAAGAGAAATACTCTACTACGCCAAATCGTT 1560
DB 1501 CAAAGACTCCAGTTAATAGAACACAGCATAAAGAGAAATACTCTACTACGCCAAATCGTT 1560

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Db 1681 GCTCAGTGAATTTGGATCTCAACCAAGCAATATGAGGAGACTCCAAAAGAAAGGGAG 1740
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Db 1741 CCAAAGTGTGGAGCCTTGAAGGGGGTGGATAGGTATCACTGTCTCACCAGGA 1800
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Db 1801 GCAAAAGGAAGGTTCTGCGCAGAGAGCGGGCCAGAGACTTAAAGCTTCACTATAATGTGA 1860
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Db 1861 CTACAACTAGATTAGTGAATCCAGATCAACTGTTTGAATGAATAATGTCTATTCTTCCAA 1920
QY 1921 AGAAGCATGTTGACTTTGTACAAAAGGTTATACACTGAAGTGTCAACACAGTCAAGTT 1980
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QY 1981 TTGGGAAAGTGACAAATGCAATTTGAATAGAGGTGCCAGCTTCAAAAACCCGATGTGG 2040
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QY 2461 TTGTGAATAT 2470
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RESULT 5

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US-10-172-118-1535
; Sequence 1535, Application US/10172118
; Publication NO. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
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; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-1175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1535
; LENGTH: 2470
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM 014791
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1535
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Query Match 100.0%; Score 2470; DB 7; Length 2470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1141 AGGCTCGGGAAAAACAGTTTCGTTTAAAGGCTTCTTCTTCTCTCTGCGCAAGCCAGTG 1200
DB 1141 AGGCTCGGGAAAAACAGTTTCGTTTAAAGGCTTCTTCTTCTCTCTGCGCAAGCCAGTG 1200
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DB 1681 GCTCAGTGGAAATGGATCTCAACCAAGCAATATGAGGAGAGATTCCTCAAAAAAGAAAGGAG 1740
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DB 1801 GCAAAAGGAAGGGTTCTGCCAGAGACGGGGCCAGAGACTAAAGCTTCACTATAATGTGA 1860
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DB 1861 CTACAACTAGATTAGTGAATCCAGATCAACTGTTTCAATGAATAATATGTTCTTCCAA 1920
QY 1921 AGAAGCATGTTGACATTTGTACAAAAGGGTTATACACTGAAGTGTCAACACAGTCAGATT 1980
DB 1921 AGAAGCATGTTGACATTTGTACAAAAGGGTTATACACTGAAGTGTCAACACAGTCAGATT 1980
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DB 1981 TTGGGAAGTGAATGCAATTTGAATTTGAAGTGTGCCAGCTTCAAAAACCGATGG 2040
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DB 2161 GGTGTGATACAGCTTACATAAAGATCTGTTATGATCGCTTTGATTTTAAAGTTCATTGGAA 2220
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DB 2281 GATATTATTTCTGTATGAATCTAAATCAAGCCCATCTGTCAATATGTTTACTGTCTTTTT 2340
QY 2341 TAAATCATGTTTGTATATTAATTAATTAATTTGTTGACCTTTCTTAGATTCATTCATATGTG 2400
DB 2341 TAAATCATGTTTGTATATTAATTAATTAATTTGTTGACCTTTCTTAGATTCATTCATATGTG 2400
QY 2401 AATGTAAAGCTTAACTATGCTCTTCTTGAATGTTAAATCTTCTTCTGAAATAAACCAT 2460
DB 2401 AATGTAAAGCTTAACTATGCTCTTCTTGAATGTTAAATCTTCTTCTGAAATAAACCAT 2460
QY 2461 TTGTGAATAT 2470
DB 2461 TTGTGAATAT 2470

RESULT 6

US-10-295-027-505
; Sequence 505, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glyme, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394

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; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 505
; LENGTH: 2470
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-505

Query Match      100.0%; Score 2470; DB 7; Length 2470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCGGGCGGAAGCGCCACACCGCGGATCGAAAGATTCTTAGGAAGCGCGTACCA 60
DB 1 TTGGCGGGCGGAAGCGCCACACCGCGGATCGAAAGATTCTTAGGAAGCGCGTACCA 60
QY 61 GCGCGTCTCTCAGGACAGCAGCGCCCTGTCTTCTGTGCGGGCGCGCTCAGCGGTGCC 120
DB 61 GCGCGTCTCTCAGGACAGCAGCGCCCTGTCTTCTGTGCGGGCGCGCTCAGCGGTGCC 120
QY 121 TCGGCGCCCTCAGGTCTCTTTCTTAATCCAAATAAACTTGCAAGAGACTATGAAGATT 180
DB 121 TCGGCGCCCTCAGGTCTCTTTCTTAATCCAAATAAACTTGCAAGAGACTATGAAGATT 180
QY 181 ATGATGAACCTTCTCAATAATATTGAATATACATGAATACTATGGACAGGTGGCTTTGCAA 240
DB 181 ATGATGAACCTTCTCAATAATATTGAATATACATGAATACTATGGACAGGTGGCTTTGCAA 240
QY 241 AGGTCAAACTTGCTGCCATATCCTTACTTGGAGAGATGGTAGCTATAAAATCATGGATA 300
DB 241 AGGTCAAACTTGCTGCCATATCCTTACTTGGAGAGATGGTAGCTATAAAATCATGGATA 300
QY 301 AAAACACACTAGGAGTGAATTTGCCCGGATCAAAACGGAGATTGAGGCTTTGAAGAACC 360
DB 301 AAAACACACTAGGAGTGAATTTGCCCGGATCAAAACGGAGATTGAGGCTTTGAAGAACC 360
QY 361 TGAGACATCAGCATATATGTCAACTTACCATGTGCTAGACAGCAGCAACAAATATTCAC 420
DB 361 TGAGACATCAGCATATATGTCAACTTACCATGTGCTAGACAGCAGCAACAAATATTCAC 420
QY 421 TGGTCTTTCAGTACTGCCCTGGAGGAGAGCTGTGTGACTATATAATTTCCAGGATCGCC 480
DB 421 TGGTCTTTCAGTACTGCCCTGGAGGAGAGCTGTGTGACTATATAATTTCCAGGATCGCC 480
QY 481 TGTCAAGAGAGAGACCGGGTGTCTTCGGTCAGATAGTATCTGCTGTGCTTATGTGC 540
DB 481 TGTCAAGAGAGAGACCGGGTGTCTTCGGTCAGATAGTATCTGCTGTGCTTATGTGC 540
QY 541 ACAGCCAGGGCTATGCTCAAGGGACCTCAAGCCAGAAATTTGCTGTTTGTATGATATC 600
DB 541 ACAGCCAGGGCTATGCTCAAGGGACCTCAAGCCAGAAATTTGCTGTTTGTATGATATC 600
QY 601 ATAAATTAAGCTGATTGACTTTGGTCTCTGTGCAAAACCCAGGGTAAACAAGGATTACC 660
DB 601 ATAAATTAAGCTGATTGACTTTGGTCTCTGTGCAAAACCCAGGGTAAACAAGGATTACC 660
QY 661 ATCTACAGACATGTGTGGGAGTCTGGCTTATGACAGCACCTGAGTTAATACAAGGCAAT 720
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661 ATCTACAGACATGTGTGGGAGTCTGGCTTATGACAGCACCTGAGTTAATACAAGGCAAT 720
721 CATATCTTGGATCAGAGGAGATGTTTGGAGCATGGGCATCTGTTATATATGTTTATGT 780
721 CATATCTTGGATCAGAGGAGATGTTTGGAGCATGGGCATCTGTTATATATGTTTATGT 780
781 GTGGATTTCTACATTTTGTATGATGATTAATGTAATGGCTTTATACAAGAGATTAAGAG 840
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841 GAAATATGATCTTCCCAAGTGGCTCTCTCCAGTAGCATCTCTCTTCTTCAACAATGC 900
901 TGCAGGTGACCCAAAGAAACGGATTCTATGAAATAATCTATTGAACCATCTCTGATCA 960
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961 TGCAGATTAACAATCTATCTGTTGAGTGGCAAGCAAGAAATCTTTTATTCACCTCGATG 1020
1021 ATGATTTGCGTAACAGAACTTTCTGTACATCAAGAAACCAAGGCAACCAATGGAGATT 1080
1021 ATGATTTGCGTAACAGAACTTTCTGTACATCAAGAAACCAAGGCAACCAATGGAGATT 1080
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1141 AGGCTCGGGGAAAAACAGTTCTTTTAAAGCTTTCTTTCTCTGTGTGCAAGCCAGTG 1200
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1201 CTACCCCATTTACAGACATCAAGTCAAAATTTGAGTCTGGAAGTGTGACCGCAAGTG 1260
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1261 ATAAAAATTTATGTGGGGATTAATAGACTATGATTTGGTGTGAAGATGATTTTCAACAG 1320
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1321 GTGCTGTACTCTCCCGAATCAAGTTTACCAAGTCTGGAAGTCAAAATCAAAATGGGTGG 1380
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1381 AATCTAAATCAATTAATCTCAGCTTTATGCAAGAACCTCTGCAAAATAAATTAAGAAACAAG 1440
1441 AAAATGTATATCTCTTAAGTCTGTATAAGAAATGAAGAGTACTTTATGTTTCTGTAGC 1500
1441 AAAATGTATATCTCTTAAGTCTGTATAAGAAATGAAGAGTACTTTATGTTTCTGTAGC 1500
1501 CAAAGACTCCAGTTAATAAGAACCCAGTGAAGAAATACTCACTACGCCAAATCGTT 1560
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1561 ACACCTACACCTCAAAAGCTAGAAAACAGTGCCTGAAAGAAACTCAATTAATAATACCAAG 1620
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1621 TAAATTTCAACAGAAACAGACAAAGTTATGACAGGTGTCTATTAGCCCTGAGAGCGGTGCC 1680
1681 GCTCAGTGGAAATGGATCTCAACCAAGCACATATGAGGAGAGACTCCAAAAGAAAGGGAG 1740
1681 GCTCAGTGGAAATGGATCTCAACCAAGCACATATGAGGAGAGACTCCAAAAGAAAGGGAG 1740
1741 CCAAGTGTGTGGAGCGCTTGAAAGGGGTGGATAAGGTTATCACTGTGTCTCACCAGGA 1800
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Db 1741 CCAAAGTGTGGAGCCTTGAAGGGGGTTGATAAGGTTTACACTGTGCTCACCAGGA 1800
Qy 1801 GCAAAAGGAGGGTCTGCAGAGACGGGCCAGAGACTAAAGCTTCACTATAATGCA 1860
Db 1801 GCAAAAGGAGGGTCTGCAGAGACGGGCCAGAGACTAAAGCTTCACTATAATGCA 1860
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Db 1861 CTACAACTAGATTAGTGAATCCAGATCAACTGTGTAATGAATAATGTCTATTCTCCAA 1920
Qy 1921 AGAAGCATGTGACTTTGTACAAAAGGGTTATACATGAAGTGTCAAAACACAGTCAGATT 1980
Db 1921 AGAAGCATGTGACTTTGTACAAAAGGGTTATACATGAAGTGTCAAAACACAGTCAGATT 1980
Qy 1981 TTGGGAAGTGAACAATGCAATTTGAATTAGAAGTGTCCAGCTTCAAAACCGATGCG 2040
Db 1981 TTGGGAAGTGAACAATGCAATTTGAATTAGAAGTGTCCAGCTTCAAAACCGATGCG 2040
Qy 2041 TGGGTATCAGGAGGCGAGCGCTTAAAGGGCGATGCCCTGGGTTTACAAAAGATTAGTGGAA 2100
Db 2041 TGGGTATCAGGAGGCGAGCGCTTAAAGGGCGATGCCCTGGGTTTACAAAAGATTAGTGGAA 2100
Qy 2101 ACATCCTATCTAGCTGCAAGGTATAATTTGATGATGCTTCCATCTCCCGGATGATG 2160
Db 2101 ACATCCTATCTAGCTGCAAGGTATAATTTGATGATGCTTCCATCTCCCGGATGATG 2160
Qy 2161 GGTGTGATACAGCTACATAAGACTGTTATGATCGCTTTGATTTAAAGTTCAATGGAA 2220
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Qy 2221 CTACCAACTTGTCTTAAAGAGCTATCTTAAAGACCAATATCTTTTGTGTTTTAAACAAA 2280
Db 2221 CTACCAACTTGTCTTAAAGAGCTATCTTAAAGACCAATATCTTTTGTGTTTTAAACAAA 2280
Qy 2281 GATATTATTTTGTGATGAATCTAAATCAAGCCCATCTGTCATATGTTACTGCTTTT 2340
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Qy 2401 AATGTAAGCTCTTAACTATCTCTTTGTAATGTGTAATTTCTTCTGAAATAAAACCAT 2460
Db 2401 AATGTAAGCTCTTAACTATCTCTTTGTAATGTGTAATTTCTTCTGAAATAAAACCAT 2460
Qy 2461 TTGTGAATAT 2470
Db 2461 TTGTGAATAT 2470

RESULT 7

US-10-173-999-126
; Sequence 126, Application US/10173999
; Publication No. US2004000563A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002420US
; CURRENT APPLICATION NUMBER: US/10/173,999
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/299,234
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/315,287
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2001-04-12

; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 126
; LENGTH: 2470
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-173-999-126

Query Match 100.0%; Score 2470; DB 7; Length 2470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGGGGCGGAGCGGCCCAACCCGGCGATFCGAAAAGATTCTTTAGGAACCCCGTACCA 60
Db 1 TTGGGGGGCGGAGCGGCCCAACCCGGCGATFCGAAAAGATTCTTTAGGAACCCCGTACCA 60
Qy 61 GCCGGTCTCTCAGACAGCAGGCCCTGTCTTCTGTGGGCGCGCTCAGCCGTGCC 120
Db 61 GCCGGTCTCTCAGACAGCAGGCCCTGTCTTCTGTGGGCGCGCTCAGCCGTGCC 120
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Db 121 TCCGCCCTCAGGTTCTTTTCTAATTCCAAATAAACTTTCGAAGAGGACTATGAAGAATT 180
Qy 181 ATGATGAACCTTCTCAAATAATTAATGAATTAATGAATTAATGAATTAATGAATTAATGA 240
Db 181 ATGATGAACCTTCTCAAATAATTAATGAATTAATGAATTAATGAATTAATGAATTAATGA 240
Qy 241 AGGTCAAACTTCCCTGCCATATCTTACTGGAGAGATGCTAGCTATAAAAATCATGGATA 300
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Qy 301 AAAACACACTAGGGAGTGAATTTGCCCGGATCAAAACGGAGATTGAGGCTTTGAAGAACC 360
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Db 421 TGGTCTTGAGTACTGCCCTGGAGAGAGCTGTTTGACTATATAATTTCCCHAGGATCGCC 480
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Qy 541 ACAGCCAGGCTATGCTCAAGGACCTCAAGCCAGAAAATTTGCTGTTGATGAATATC 600
Db 541 ACAGCCAGGCTATGCTCAAGGACCTCAAGCCAGAAAATTTGCTGTTGATGAATATC 600
Qy 601 ATAAATTAAGCTGATTGACTTTGGTCTGTGTGCAAAACCCCAAGGTAACAAGGATATCC 660
Db 601 ATAAATTAAGCTGATTGACTTTGGTCTGTGTGCAAAACCCCAAGGTAACAAGGATATCC 660
Qy 661 ATCTACAGACATGCTGTGGAGTCTGGCTTATGACGACCTGAGTTAATAACAAGGCAAT 720
Db 661 ATCTACAGACATGCTGTGGAGTCTGGCTTATGACGACCTGAGTTAATAACAAGGCAAT 720
Qy 721 CATATCTTGGATCAGAGGAGATGTTTGGAGCATGGGCATCTGTTATATGTTCTTATGT 780
Db 721 CATATCTTGGATCAGAGGAGATGTTTGGAGCATGGGCATCTGTTATATGTTCTTATGT 780
Qy 781 GTGGATTTCTACATTTGATGATGATGTAATGTAATGCTTTTATACAGAGATATCAGAG 840
Db 781 GTGGATTTCTACATTTGATGATGATGTAATGTAATGCTTTTATACAGAGATATCAGAG 840
Qy 841 GAAAATATGATGTTCCCAAGTGGCTCTCTCCAGTAGCATTTCTGCTTCTTCAACAATGC 900
Db 841 GAAAATATGATGTTCCCAAGTGGCTCTCTCCAGTAGCATTTCTGCTTCTTCAACAATGC 900
Qy 901 TGCAGGTGGACCCAAAGAAACGGATTTTCTATGAAAAATCTATTGAACCATCCCTGGATCA 960

Db 901 ||||| TGCAAGTGGACCCAAAGAAACGGAATTCATATGAAAAATCTATTTGAACCATCCCTGGATCA 960
QY 961 TGCAAGATTAACAATCTCTCTGTTGAGTGGCAAGCAAGAAATCCTTTATTTACCTCGATG 1020
Db 961 TGCAAGATTAACAATCTCTCTGTTGAGTGGCAAGCAAGAAATCCTTTATTTACCTCGATG 1020
QY 1021 ATGATTCGGTAAACAGAACTTCTGTCATCATACAGAAACAAACAGGCAAAACAATGGAGATT 1080
Db 1021 ATGATTCGGTAAACAGAACTTCTGTCATCATACAGAAACAAACAGGCAAAACAATGGAGATT 1080
QY 1081 TAATTTCACTGTCGGAGTAGATCACTCACGGCTACCTATCTTCTGCTCTAGCCAA 1140
Db 1081 TAATTTCACTGTCGGAGTAGATCACTCACGGCTACCTATCTTCTGCTCTAGCCAA 1140
QY 1141 AGCTCGGGGAAACCAAGTTTCGTTTAAGGCTTCTCTCTCTCTGTCGACCAAGCCAGTG 1200
Db 1141 AGCTCGGGGAAACCAAGTTTCGTTTAAGGCTTCTCTCTCTCTGTCGACCAAGCCAGTG 1200
QY 1201 CTACCCCATTCACAGACATCAAGTCAAAATTAATTTGGAGTCTGGAAGATGTGACCGCAAGTG 1260
Db 1201 CTACCCCATTCACAGACATCAAGTCAAAATTAATTTGGAGTCTGGAAGATGTGACCGCAAGTG 1260
QY 1261 ATAAAAATTAATGCGGGGATTAATAGACTATGATTTGTTGTTGAGATGATTTATCAACAG 1320
Db 1261 ATAAAAATTAATGCGGGGATTAATAGACTATGATTTGTTGTTGAGATGATTTATCAACAG 1320
QY 1321 GTGCTGCTACTCCCGAAACATACAGTTTACCAAGTACTGGACAGAAATCAATGGGGTGG 1380
Db 1321 GTGCTGCTACTCCCGAAACATACAGTTTACCAAGTACTGGACAGAAATCAATGGGGTGG 1380
QY 1381 AATCTAAATCATTAATCCAGCCTTATGAGAAACACCTGCAAAATAAATTAAGAAACAAAG 1440
Db 1381 AATCTAAATCATTAATCCAGCCTTATGAGAAACACCTGCAAAATAAATTAAGAAACAAAG 1440
QY 1441 AAAATGTATATCTCTTAAGTCTGCTGTAAGAAATGAAGTACTTTATGTTCTCTGAGC 1500
Db 1441 AAAATGTATATCTCTTAAGTCTGCTGTAAGAAATGAAGTACTTTATGTTCTCTGAGC 1500
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Db 1501 CAAAGACTCCAGTTAATAAGAACCCAGCAATAGAGAGAAATCTCACTACGCCAAATCGTT 1560
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Db 1621 TAAATTCACAGGAACAGACAGATTAATGACAGGTCTATTAGCCCTGAGAGCGGTGCC 1680
QY 1681 GCTCAGTGGAAATGGATCTCAACCAAGCACATATGGAGAGACTCCCAAAAGAAAGGGAG 1740
Db 1681 GCTCAGTGGAAATGGATCTCAACCAAGCACATATGGAGAGACTCCCAAAAGAAAGGGAG 1740
QY 1741 CCAAAGTGTGAGAGCTTGAAGGGGTGGATAAGGTTTACTGTGCTCACCAGGA 1800
Db 1741 CCAAAGTGTGAGAGCTTGAAGGGGTGGATAAGGTTTACTGTGCTCACCAGGA 1800
QY 1801 GCAAAAGGAAGGGTCTGCGAGAGACGGGCCCGAGAGACTTAAAGCTTCACTATAATGTGA 1860
Db 1801 GCAAAAGGAAGGGTCTGCGAGAGACGGGCCCGAGAGACTTAAAGCTTCACTATAATGTGA 1860
QY 1861 CTACAACTAGATTAGTGAATCCAGATCAACTGTTGAATGAATGAATGCTATTCTTCCAA 1920
Db 1861 CTACAACTAGATTAGTGAATCCAGATCAACTGTTGAATGAATGAATGCTATTCTTCCAA 1920
QY 1921 AGAAGCATGTTGACTTTGTACAAAAGGGTTATACACTGAAGTGTCAAAACACAGTCAGATT 1980
Db 1921 AGAAGCATGTTGACTTTGTACAAAAGGGTTATACACTGAAGTGTCAAAACACAGTCAGATT 1980
QY 1981 TTGGGAAAGTGAACATGCAATTTGAATTAAGAGTGTGCCAGCTTCAAAAACCCGATGTGG 2040
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Db 1981 TTGGGAAAGTGAACATGCAATTTGAATTAAGAGTGTGCCAGCTTCAAAAACCCGATGTGG 2040
QY 2041 TTGGGATCAGGAGGCGAGCGGCTTAAGGCGGATGCTCTGGGTTTACAAAAGATTAGTGGAA 2100
Db 2041 TTGGGATCAGGAGGCGAGCGGCTTAAGGCGGATGCTCTGGGTTTACAAAAGATTAGTGGAA 2100
QY 2101 ACATCCTATCTAGCTGCAAGGTTAATTTGATGATTTCTTCCATCCTGCCGGATGAGTGTG 2160
Db 2101 ACATCCTATCTAGCTGCAAGGTTAATTTGATGATTTCTTCCATCCTGCCGGATGAGTGTG 2160
QY 2161 GGTGTGATACAGCTACATAAAGACCTGTTATGATCGTTTGAATTTTAAAGTTTCATTGGAA 2220
Db 2161 GGTGTGATACAGCTACATAAAGACCTGTTATGATCGTTTGAATTTTAAAGTTTCATTGGAA 2220
QY 2221 CTACCAACTTGTGTTCTAAAGAGCTATCTTAAGACCAATATCTCTTTGTTTTTAAACAAAA 2280
Db 2221 CTACCAACTTGTGTTCTTAAGAGCTATCTTAAGACCAATATCTCTTTGTTTTTAAACAAAA 2280
QY 2281 GATATATTTTGTGTATGAATCTAAATCAAGCCCATCTGTCAATATGTTACTGTCTTTTT 2340
Db 2281 GATATATTTTGTGTATGAATCTAAATCAAGCCCATCTGTCAATATGTTACTGTCTTTTT 2340
QY 2341 TAATCATGTGTTTGTATATTAATAATTTGTTGACTTTCTTAGATTCACTTCCATATGTG 2400
Db 2341 TAATCATGTGTTTGTATATTAATAATTTGTTGACTTTCTTAGATTCACTTCCATATGTG 2400
QY 2401 AATGTAAGCTCTTAACATGCTCTTTGTAATGTTGTAATTTCTTCTGAAATAAAACCAT 2460
Db 2401 AATGTAAGCTCTTAACATGCTCTTTGTAATGTTGTAATTTCTTCTGAAATAAAACCAT 2460
QY 2461 TTGTGAATAT 2470
Db 2461 TTGTGAATAT 2470

RESULT 8

US-10-342-887-1535
; Sequence 1535, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1535
; LENGTH: 2470
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1535

Query Match 100.0%; Score 2470; DB 8; Length 2470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGGCGGCGGAAGCGGCCACACCGCGGATTCGAAAGATTCTTAGGAACCCCGTACCA 60
Db 1 TTGGCGGCGGAAGCGGCCACACCGCGGATTCGAAAGATTCTTAGGAACCCCGTACCA 60
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Db 121 TCGCGCCCTCAGGTTCTTTTCTAATTCGAATTAATCTTGAAGAGATT 180
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Db 181 ATGATGAATCTTCAATATATATGAATACATGAATCTATTTGGGACAGGTTGGTTCGAA 240
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Db 241 AGGTCAAACTTGCCTGCCATATCTTTACTTGGAGAGATGGTAGCTATAAAATCATGGATA 300
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Db 301 AAAACACATAGGAGATGATTTGCCCGGATCAAAACGGAGATTGAGGCCCTTGAAGAACC 360
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QY 421 TGGTTCTTGAGTACTGCCCTGGAGGAGCTGTTTGACTATATAATTTCCAGGATCGCC 480
Db 421 TGGTTCTTGAGTACTGCCCTGGAGGAGCTGTTTGACTATATAATTTCCAGGATCGCC 480
QY 481 TGTGAGAAGAGAGACCGGGTGTCTTCCGTGAGATAGTATCTGCTGTGCTTTATGTGC 540
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QY 541 ACAGCCAGGCTATGCTCAGAGGACCTCAAGCCAGGAATTTGCTTTGATGAATATC 600
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Db 721 CATATCTTGATCAGAGGACAGATTTTGGAGCATGSCATCTGTTATATGTTCTTATGT 780
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RESULT 9
US-10-656-598-1
; Sequence 1, Application US/10656598
; Publication No. US20040229232A1
; GENERAL INFORMATION:
; APPLICANT: DAVID P. DAVIS
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: WILLIAM I. WOOD
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P1981R1P1-US
; CURRENT APPLICATION NUMBER: US/10/656,598
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: US 60/410,166
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 1
; LENGTH: 2470
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-656-598-1

Query Match 100.0%; Score 2470; DB 9; Length 2470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2461 TTGTGAATAT 2470
Db 2461 TTGTGAATAT 2470
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RESULT 10

US-10-723-860-2443

; Sequence 2443, Application US/10723860

; Publication No. US20040253606A1

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; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2443
; LENGTH: 2470
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2443
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Query Match 100.0%; Score 2470; DB 9; Length 2470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2341 TAAATCATGTGGTTTTGTATATTAATTAATTAATGTTGACTTTCTTAGATTTCACTTCCATATGTG 2400
Db 2341 TAAATCATGTGGTTTTGTATATTAATTAATTAATGTTGACTTTCTTAGATTTCACTTCCATATGTG 2400
Qy 2401 AATGTAAGCTTTAACTACTGCTCTTTGTAATGTTGTAATTTCTTTCTGAAATAAAACCAT 2460
Db 2401 AATGTAAGCTTTAACTACTGCTCTTTGTAATGTTGTAATTTCTTTCTGAAATAAAACCAT 2460
Qy 2461 TTGTGAATAT 2470
Db 2461 TTGTGAATAT 2470
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RESULT 11

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US-10-848-755A-169
; Sequence 169, Application US/10848755A
; Publication No. US20050054826A1
; GENERAL INFORMATION:
; APPLICANT: Mao, Mao
; TITLE OF INVENTION: HUMAN DIAPHANOUS-3 GENE AND METHODS OF USE THEREFOR
; FILE REFERENCE: 9301-196-999
; CURRENT APPLICATION NUMBER: US/10/848,755A
; CURRENT FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: 60/471,842
; PRIOR FILING DATE: 2003-05-11
; NUMBER OF SEQ ID NOS: 275
; SOFTWARE: PatentIn version 3.2 CAM: 301891-999188
; SEQ ID NO 169
; LENGTH: 2470
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-848-755A-169
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Query Match 100.0%; Score 2470; DB 10; Length 2470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 TTGGCGGGCGGAAGCGGCCACACCCGGCGATCGAAAGATTTCTTAGNACGCCCTACCA 60
Db 1 TTGGCGGGCGGAAGCGGCCACACCCGGCGATCGAAAGATTTCTTAGNACGCCCTACCA 60
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Qy	61	GC	CG	CGT	CT	CT	C	A	G	G	A	C	A	G	C	C	C	C	T	G	C	T	T	T	G	T	G	G	G	C	G	C	T	C	A	G	C	G	T	G	C	C	120									
Db	61	GC	CG	GT	CT	CT	C	A	G	A	C	A	G	C	A	G	C	C	C	T	G	C	T	T	T	G	T	G	G	G	C	G	C	T	C	A	G	C	G	T	G	C	C	120								
Qy	121	TC	GC	CC	CC	CT	C	A	G	G	T	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	180										
Db	121	TC	GC	CC	CT	CAG	GT	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	180										
Qy	181	AT	GA	T	GA	A	C	T	T	C	A	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	240										
Db	181	AT	GA	T	GA	A	C	T	T	C	A	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	240										
Qy	241	AG	GT	C	A	A	C	T	T	G	C	T	G	C	A	T	A	T	C	T	G	A	G	A	T	G	T	A	G	T	A	T	A	A	A	A	T	C	A	T	G	A	300									
Db	241	AG	GT	C	A	A	C	T	T	G	C	C	A	T	A	T	C	T	T	A	C	T	G	A	G	A	T	G	T	A	T	A	A	A	A	T	C	A	T	G	A	300										
Qy	301	A	A	A	C	A	C	A	T	A	G	G	A	G	T	T	T	T	G	C	C	C	G	G	A	T	C	A	A	A	C	G	G	A	T	T	G	A	G	C	C	T	C	A	360							
Db	301	A	A	A	C	A	C	A	T	A	G	G	A	G	T	T	T	T	G	C	C	C	G	G	A	T	C	A	A	A	C	G	G	A	T	T	G	A	G	C	C	T	C	A	360							
Qy	361	T	G	A	C	A	T	A	G	C	A	T	A	T	A	T	G	T	C	A	A	C	T	C	A	T	G	T	G	C	T	A	G	A	C	A	G	C	A	A	A	A	T	T	C	A	420					
Db	361	T	G	A	C	A	T	A	G	C	A	T	A	T	A	T	G	T	C	A	A	C	T	C	A	T	G	T	G	C	T	A	G	A	C	A	G	C	A	A	A	A	T	T	C	A	420					
Qy	421	T	G	G	T	C	T	T	G	A	G	T	A	G	C	T	G	G	A	G	A	G	C	T	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	480									
Db	421	T	G	G	T	C	T	T	G	A	G	T	A	G	C	T	G	G	A	G	A	G	C	T	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	480									
Qy	481	T	G	T	C	A	G	A	G	A	G	A	C	C	G	G	G	T	C	T	T	C	G	T	C	A	G	A	T	A	G	T	A	T	C	G	T	T	T	T	T	T	T	540								
Db	481	T	G	T	C	A	G	A	G	A	G	A	C	C	G	G	G	T	C	T	T	C	G	T	C	A	G	A	T	A	G	T	A	T	C	G	T	T	T	T	T	T	T	540								
Qy	541	A	C	A	C	C	A	G	G	C	T	A	G	G	A	C	T	C	A	A	G	C	C	T	C	A	A	G	C	C	A	A	A	A	T	T	G	C	T	T	T	G	A	T	C	600						
Db	541	A	C	A	C	C	A	G	G	C	T	A	G	G	A	C	T	C	A	A	G	C	C	T	C	A	A	G	C	C	A	A	A	A	T	T	G	C	T	T	T	G	A	T	C	600						
Qy	601	A	T	A	A	T	T	A	A	G	C	T	A	G	C	T	T	T	G	G	T	C	T	C	T	G	C	A	A	A	A	C	C	A	A	G	G	T	A	A	C	A	A	G	A	T	P	A	C	660		
Db	601	A	T	A	A	T	T	A	A	G	C	T	A	G	C	T	T	T	G	G	T	C	T	C	T	G	C	A	A	A	A	C	C	A	A	G	G	T	A	A	C	A	A	G	A	T	P	A	C	660		
Qy	661	A	T	C	A	C	A	G	A	C	A	T	G	C	T	G	G	A	G	T	C	T	G	C	T	A	T	G	C	A	C	C	T	G	A	G	T	T	A	A	T	C	A	A	G	G	C	A	A	A	T	720
Db	661	A	T	C	A	C	A	G	A	C	A	T	G	C	T	G	G	A	G	T	C	T	G	C	T	A	T	G	C	A	C	C	T	G	A	G	T	T	A	A	T	C	A	A	G	G	C	A	A	A	T	720
Qy	721	C	A	T	A	T	C	T	T	G	A	T	C	A	G	A	G	C	A	G	A	T	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	780							
Db	721	C	A	T	A	T	C	T	T	G	A	T	C	A	G	A	G	C	A	G	A	T	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	780							
Qy	781	G	T	G	A	T	T	C	A	C	T	T	G	A	T	A	T	G	A	T	T	G	G	T	T	T	A	T	A	T	A	T	A	T	A	C	A	A	G	A	A	T	A	T	C	A	G	A	840			
Db	781	G	T	G	A	T	T	C	A	C	T	T	G	A	T	A	T	G	A	T	T	G	G	T	T	T	A	T	A	T	A	T	A	T	A	C	A	A	G	A	A	T	A	T	C	A	G	A	840			
Qy	841	G	A	A	A	T	A	T	A	G	T	T	C	C	A	G	T	G	C	T	C	C	C	A	G	T	A	G	A	T	T	C	C	C	A	G	T	A	G	A	T	T	C	A	A	A	T	G	C	900		
Db	841	G	A	A	A	T	A	T	A	G	T	T	C	C	A	G	T	G	C	T	C	C	C	A	G	T	A	G	A	T	T	C	C	C	A	G	T	A	G	A	T	T	C	A	A	A	T	G	C	900		
Qy	901	T	G	C	A	G	G	T	G	A	C	C	A	A	G	A	A	C	G	G	A	T	T	C	T	A	T	G	A	A	A	A	T	C	T	A	T	T	G	A	A	C	C	C	C	T	G	A	T	C	A	960
Db	901	T	G	C	A	G	G	T	G	A	C	C	A	A	G	A	A	C	G	G	A	T	T	C	T	A	T	G	A	A	A	A	T	C	T	A	T	T	G	A	A	C	C	C	C	T	G	A	T	C	A	960
Qy	961	T	G	C	A	G	A	T	T	A	C	A	A	T	A	T	C	T	C	T	G	A	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	1020					
Db	961	T	G	C	A	G	A	T	T	A	C	A	A	T	A	T	C	T	C	T	G	A	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	1020					
Qy	1021	A	T	G	A	T	T	G	G	T	A	C	A	A	A	T	T	T	C	T	G	T	A	C	A	T	C	A	C	A	A	A	A	C	A	A	C	A	A	C	A	A	A	A	T	T	G	A	G	A	T	1080
Db	1021	A	T	G	A	T	T	G	G	T	A	C	A	A	A	T	T	T	C	T	G	T	A	C	A	T	C	A	C	A	A	A	A	C	A	A	C	A	A	A	A	T	T	G	A	G	A	T	1080			
Qy	1081	T	A	A	T	T	C	A	C	T	G	G	C	A	G	T	A	T	C	A	C	C	T	C	A	C	C	T	C	A	C	C	T	C	A	C	C	T	C	A	C	C	T	C	A	C	A	1140				
Db	1081	T	A	A	T	T	C	A	C	T	G	G	C	A	G	T	A	T	C	A	C	C	T	C	A	C	C	T	C	A	C	C	T	C	A	C	C	T	C	A	C	C	T	C	A	C	A	1140				

1141	Qy	AGCCTCGGGAAAAACAGTTCGTTTAAAGCGTTCTTCTTTCTCCTCTGCAACGCGAGTG	1200
1141	Db	AGCCTCGGGAAAAACAGTTCGTTTAAAGCGTTCTTCTTTCTCCTCTGCAACGCGAGTG	1200
1201	Qy	CTACCCCATTTACAGACATCAAGTCAATAAATTTGGAGTCTGGAAAGATGTGACCGCAAGTG	1260
1201	Db	CTACCCCATTTACAGACATCAAGTCAATAAATTTGGAGTCTGGAAAGATGTGACCGCAAGTG	1260
1261	Qy	ATAAAAATTATGTGGCGGATTTAATAAGACTATAGATTTGGTGTGAAGATGATTTATCAACAG	1320
1261	Db	ATAAAAATTATGTGGCGGATTTAATAAGACTATAGATTTGGTGTGAAGATGATTTATCAACAG	1320
1321	Qy	GTGCTGCTACTCCCGAAACATACAGTTTACCAAGTCTGGACAGAAATCAAAATGGGGTGG	1380
1321	Db	GTGCTGCTACTCCCGAAACATACAGTTTACCAAGTCTGGACAGAAATCAAAATGGGGTGG	1380
1381	Qy	AATCTAAATCATTAACCTCCAGCCTTATGCAGAAACACCTCGCAATAAATTAAGAAACAAAG	1440
1381	Db	AATCTAAATCATTAACCTCCAGCCTTATGCAGAAACACCTCGCAATAAATTAAGAAACAAAG	1440
1441	Qy	AAAATGTATATCTCTTAAGTCTGCTGTAAAGAAATGAAGATGACTTTATGTTTCCCTGAGC	1500
1441	Db	AAAATGTATATCTCTTAAGTCTGCTGTAAAGAAATGAAGATGACTTTATGTTTCCCTGAGC	1500
1501	Qy	CAAAGACTCCAGTPTAATAAGAACACAGCATTAAGAGAGAAATCACTCACTAGCCCAAAATCGTT	1560
1501	Db	CAAAGACTCCAGTPTAATAAGAACACAGCATTAAGAGAGAAATCACTCACTAGCCCAAAATCGTT	1560
1561	Qy	ACACTACACCTCCAAAGCTTAGAAACACAGTGCCTGAAAGAAATCCAAATTAATAATACCAG	1620
1561	Db	ACACTACACCTCCAAAGCTTAGAAACACAGTGCCTGAAAGAAATCCAAATTAATAATACCAG	1620
1621	Qy	TAAATTTCAACAGAAACAGCAAGTTAATGACAGGTGCTCATTTAGCCCTGAGAGCGGTGCC	1680
1621	Db	TAAATTTCAACAGAAACAGCAAGTTAATGACAGGTGCTCATTTAGCCCTGAGAGCGGTGCC	1680
1681	Qy	GCTCAGTGGAAATTTGGATCTCAACCAACAGCATATGGAGGAGACTTCCAAAAGAAAGGGAG	1740
1681	Db	GCTCAGTGGAAATTTGGATCTCAACCAACAGCATATGGAGGAGACTTCCAAAAGAAAGGGAG	1740
1741	Qy	CCAAAGTGTGGAGCCTTGAAGGGGGTTGATAAGTTATCACTGTCTCAACCGA	1800
1741	Db	CCAAAGTGTGGAGCCTTGAAGGGGGTTGATAAGTTATCACTGTCTCAACCGA	1800
1801	Qy	GCAAAAGGAAGGCTTCTGCCAGAGAAGGGGCCAGAGAATAAAGCTTCACTAATAATGTGA	1860
1801	Db	GCAAAAGGAAGGCTTCTGCCAGAGAAGGGGCCAGAGAATAAAGCTTCACTAATAATGTGA	1860
1861	Qy	CTACAACCTAGATTTAGTGAATCCAGATCAACTGTTTGAATGAAATAATGTCTATTCTTCCAA	1920
1861	Db	CTACAACCTAGATTTAGTGAATCCAGATCAACTGTTTGAATGAAATAATGTCTATTCTTCCAA	1920
1921	Qy	AGAAAGCATTTGACTTTGTACAAAAGGGTTATACACTGAAGTGTCAAAACACAGTCAGATT	1980
1921	Db	AGAAAGCATTTGACTTTGTACAAAAGGGTTATACACTGAAGTGTCAAAACACAGTCAGATT	1980
1981	Qy	TTGGGAAAGTGACAAATGCAATTTGAATTTAGAAGTGTGCCAGTTCAAAAACCCGATGTGG	2040
1981	Db	TTGGGAAAGTGACAAATGCAATTTGAATTTAGAAGTGTGCCAGTTCAAAAACCCGATGTGG	2040
2041	Qy	TGGGTATCAGGAGGACGGCCTTAAGGCCATCGCTGGGTTTACAAAAGATTTAGTGAAG	2100
2041	Db	TGGGTATCAGGAGGACGGCCTTAAGGGCGATGCTGGGTTTACAAAAGATTTAGTGAAG	2100
2101	Qy	ACATCCTATCTAGCTGCAAGGTATTAATGTAGATTTCTCCATCCTGCCGGATGAGTGTG	2160
2101	Db	ACATCCTATCTAGCTGCAAGGTATTAATGTAGATTTCTTCCATCCTGCCGGATGAGTGTG	2160
2161	Qy	GGTGTGATACAGCCTACATAAAGACTGTTTATGATTCGCTTTTGAATTTAAAGTTCATTGGA	2220
2161	Db	GGTGTGATACAGCCTACATAAAGACTGTTTATGATTCGCTTTTGAATTTAAAGTTCATTGGA	2220
2221	Qy	CTACCAACTTTGTTCTTAAAGAGCTATCTTAAGACCAATATCTCTTTGTTTTTAAACAAA	2280

Db 1201 CTACCCATTACAGACATCAAGTCAAAATAATTGGAGTCTGGAAGATGTGACCGCAAGTG 1260
Qy 1261 ATAAATAATTATGTGGCGGATTAATAGACTATGATTGGTGTGAAGATGATTATCAACAG 1320
Db 1261 ATAAATAATTATGTGGCGGATTAATAGACTATGATTGGTGTGAAGATGATTATCAACAG 1320
Qy 1321 GTGCTGCTACTCCCGGAACATCACAGTTTACCAAGTACTGGACAGAAATCAAAATGGGGTG 1380
Db 1321 GTGCTGCTACTCCCGGAACATCACAGTTTACCAAGTACTGGACAGAAATCAAAATGGGGTG 1380
Qy 1381 AATCTAAATCATTAATCTCAGCCTTATGCGAAGACACCTGCAAAATAAAATTAAGAACAAAG 1440
Db 1381 AATCTAAATCATTAATCTCAGCCTTATGCGAAGACACCTGCAAAATAAAATTAAGAACAAAG 1440
Qy 1441 AAAATGTATATCTCTCTAGTCTGCTGTAAGAAATCAAGAGTACTTTATGTTTCTCTGAGC 1500
Db 1441 AAAATGTATATCTCTCTAGTCTGCTGTAAGAAATCAAGAGTACTTTATGTTTCTCTGAGC 1500
Qy 1501 CAAAGACTCCAGTTAATAAGAACCCAGCATAAGAGAGAAATACTCACTACGCCAAATCGTT 1560
Db 1501 CAAAGACTCCAGTTAATAAGAACCCAGCATAAGAGAGAAATACTCACTACGCCAAATCGTT 1560
Qy 1561 ACACACACCTCAAAAGCTAGAAACGAGTCCCTGAAAGAACTCCAATTAATAATACAG 1620
Db 1561 ACACACACCTCAAAAGCTAGAAACGAGTCCCTGAAAGAACTCCAATTAATAATACAG 1620
Qy 1621 TAAATTCACNGAACAGACAGTAAATGACAGGTCTATTAGCCCTGAGAGCGGTGCC 1680
Db 1621 TAAATTCACNGAACAGACAGTAAATGACAGGTCTATTAGCCCTGAGAGCGGTGCC 1680
Qy 1681 GCTCAGTGGAAATTTGGATCTCAACCAAGCACATATGAGGAGACTCCAAAGAAAGAGGAG 1740
Db 1681 GCTCAGTGGAAATTTGGATCTCAACCAAGCACATATGAGGAGACTCCAAAGAAAGAGGAG 1740
Qy 1741 CCAAGTGTGTGGAGCCTTGAAGGGGTGGATAAGGTATCACTGTGCTCACAGGA 1800
Db 1741 CCAAGTGTGTGGAGCCTTGAAGGGGTGGATAAGGTATCACTGTGCTCACAGGA 1800
Qy 1801 GCAAAAGGAGGGTCTGCCAGAGACGGGCCAGAGACTTAAAGCTTCACTATAATGTGA 1860
Db 1801 GCAAAAGGAGGGTCTGCCAGAGACGGGCCAGAGACTTAAAGCTTCACTATAATGTGA 1860
Qy 1861 CTACAACTAGATTAAGTGAATCCAGATCAACTGTGTGAATGAATAATGTCTATTCTTCCAA 1920
Db 1861 CTACAACTAGATTAAGTGAATCCAGATCAACTGTGTGAATGAATAATGTCTATTCTTCCAA 1920
Qy 1921 AGAAGCATGTGTGACTTTGTACAAAAGGGTTATACATGAAGTGTCAAAACACAGTCAAGTT 1980
Db 1921 AGAAGCATGTGTGACTTTGTACAAAAGGGTTATACATGAAGTGTCAAAACACAGTCAAGTT 1980
Qy 1981 TTGGGAAAGTGCAATGCAATTTGAATTAAGAGTGTCCAGCTTCAAAAACCCGATGTGG 2040
Db 1981 TTGGGAAAGTGCAATGCAATTTGAATTAAGAGTGTCCAGCTTCAAAAACCCGATGTGG 2040
Qy 2041 TGGGTATCAGGAGCGAGCGCTTAAAGCGATCCCTGGGTTTACAAAAGATTAAGTGTGG 2100
Db 2041 TGGGTATCAGGAGCGAGCGCTTAAAGCGATCCCTGGGTTTACAAAAGATTAAGTGTGG 2100
Qy 2101 ACATCCTATCTAGCTGCAAGGTATAATGTAGTGAATCTTCCATCCTGCCGATGAGTGTG 2160
Db 2101 ACATCCTATCTAGCTGCAAGGTATAATGTAGTGAATCTTCCATCCTGCCGATGAGTGTG 2160
Qy 2161 GGTGTGATACAGCCTACATAAGACGTGTATATGATCGCTTTGATTTTAAAGTTTCATTTGGA 2220
Db 2161 GGTGTGATACAGCCTACATAAGACGTGTATATGATCGCTTTGATTTTAAAGTTTCATTTGGA 2220
Qy 2221 CTACCAACTTGTGTCTAAAGAGCTATCTTAAAGCAATATCTCTTTGTTTTTAAACAAA 2280
Db 2221 CTACCAACTTGTGTCTAAAGAGCTATCTTAAAGCAATATCTCTTTGTTTTTAAACAAA 2280
Qy 2281 GATATTAATTTGTGTATGAATCTAAATCAAGCCCATCTGCTATTAATGTTACTGTCTTTT 2340
Db 2281 GATATTAATTTGTGTATGAATCTAAATCAAGCCCATCTGCTATTAATGTTACTGTCTTTT 2340

Qy 2341 TAATCATGTGTTTTGTATATTAATAATTTGTGACTTTCTTAGATTCACCTCCATATGTG 2400
Db 2341 TAATCATGTGTTTTGTATATTAATAATTTGTGACTTTCTTAGATTCACCTCCATATGTG 2400
Qy 2401 AATGTAAGCTCTTAACATATGCTCTTTGTAAATGTGTAATTTCTTGAATAAAACCAT 2460
Db 2401 AATGTAAGCTCTTAACATATGCTCTTTGTAAATGTGTAATTTCTTCTGAAATAAAACCAT 2460
Qy 2461 TTGTGAATAT 2470
Db 2461 TTGTGAATAT 2470

RESULT 13

US-10-756-149-2259
; Sequence 2259, Application US/10756149
; Publication NO. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2259
; LENGTH: 2470
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-756-149-2259

Query Match 100.0%; Score 2470; DB 10; Length 2470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGCGGGCGGAAGCGGCCACAAACCCGGCGATCGAAAGATTCTTAGGAACGCCGTACCA 60
Db 1 TTGGCGGGCGGAAGCGGCCACAAACCCGGCGATCGAAAGATTCTTAGGAACGCCGTACCA 60
Qy 61 GCCCGCTCTCAGAACAGCAGCGCCCTGTCTTCTGTGGCGCGCTCAGCGTGGCC 120
Db 61 GCCCGCTCTCAGAACAGCAGCGCCCTGTCTTCTGTGGCGCGCTCAGCGTGGCC 120
Qy 121 TCGGCCCTCAGGTTCTTTTCTTAATCCAAATAAATGCAAGAGACTATGAAGATT 180
Db 121 TCGGCCCTCAGGTTCTTTTCTTAATCCAAATAAATGCAAGAGACTATGAAGATT 180
Qy 181 ATGATGAACCTCTCAAAATATTAATGAATTAACATGAACCTATTGGGACAGGTGGCTTTGCAA 240
Db 181 ATGATGAACCTCTCAAAATATTAATGAATTAACATGAACCTATTGGGACAGGTGGCTTTGCAA 240
Qy 241 AGGTCAAACTTGCCTGCCATATCTTCTTCTGAGAGATGCTAGCTATAAAAAATCATGGATA 300
Db 241 AGGTCAAACTTGCCTGCCATATCTTCTTCTGAGAGATGCTAGCTATAAAAAATCATGGATA 300
Qy 301 AAAACACACTAGGAGTGAATTTGCCCGGATCAAAACCGAGATTGAGGCTTTGAAGAACC 360
Db 301 AAAACACACTAGGAGTGAATTTGCCCGGATCAAAACCGAGATTGAGGCTTTGAAGAACC 360
Qy 361 TGAGACATCAGCATATATGTCAACTCTACACTGTGTAGAGACAGCAACAAAATATTCA 420
Db 361 TGAGACATCAGCATATATGTCAACTCTACACTGTGTAGAGACAGCAACAAAATATTCA 420
Qy 421 TGGTCTTCAGTACTGCGCTCGAGGAGCTGTTTGAATATATTAATTTCCAGGATCGCC 480
Db 421 TGGTCTTCAGTACTGCGCTCGAGGAGCTGTTTGAATATATTAATTTCCAGGATCGCC 480
Qy 481 TGTCAAGAGAGAGACCGCGGTTGTCTCCGTCAAGTACTGTCTGTGTTGCTTATGTGC 540
Db 481 TGTCAAGAGAGAGACCGCGGTTGTCTCCGTCAAGTACTGTCTGTGTTGCTTATGTGC 540

Qy	541	ACGCCAGGGCTATGCTCACAAGGGAACCTCAAGCCAGAAAAATTTGCTGTTGATGAAATATC	600
Db	541	ACGCCAGGGCTATGCTCACAAGGGAACCTCAAGCCAGAAAAATTTGCTGTTGATGAAATATC	600
Qy	601	ATAAATTAAAGCTGATTGACATTTGGTCTCTGTGCAAAACCCCAAGGTAACCAAGGATTACC	660
Db	601	ATAAATTAAAGCTGATTGACATTTGGTCTCTGTGCAAAACCCCAAGGTAACCAAGGATTACC	660
Qy	661	ATCTACAGACATGCTGGGAGTCTGGCTTATGCAGCACCTGAGTTAATAACAAGGCAAAAT	720
Db	661	ATCTACAGACATGCTGGGAGTCTGGCTTATGCAGCACCTGAGTTAATAACAAGGCAAAAT	720
Qy	721	CATATCTTGGATCAGAGCAGATGTTTGGAGCATGCGGCATCTGTTATATGTTCTTATGT	780
Db	721	CATATCTTGGATCAGAGCAGATGTTTGGAGCATGCGGCATCTGTTATATGTTCTTATGT	780
Qy	781	GTGGATTTCTACCATTTGATCATGATTAATGTAAATGGCTTTATACAAGAAGATTATGAGAG	840
Db	781	GTGGATTTCTACCATTTGATCATGATTAATGTAAATGGCTTTATACAAGAAGATTATGAGAG	840
Qy	841	GAAATATGATGTTTCCCAAGTGGCTCTCCAGTAGCATTTCTGCTTCTTCAACAAATGC	900
Db	841	GAAATATGATGTTTCCCAAGTGGCTCTCCAGTAGCATTTCTGCTTCTTCAACAAATGC	900
Qy	901	TGCAGGTGGACCCAAAGAAACCGAATTTCTATGAAAAATCTATTGAAACATCCCTGGATCA	960
Db	901	TGCAGGTGGACCCAAAGAAACCGAATTTCTATGAAAAATCTATTGAAACATCCCTGGATCA	960
Qy	961	TGCAAGATTACAACTATCTCTGTGAGTGGCAAGCAAGATTCCTTTATTTCACCTCGATG	1020
Db	961	TGCAAGATTACAACTATCTCTGTGAGTGGCAAGCAAGATTCCTTTATTTCACCTCGATG	1020
Qy	1021	ATGATTTGGTAAACAGAACTTTCTGTACATCAACAGAAACAAAGCAACCAATGGAGGATT	1080
Db	1021	ATGATTTGGTAAACAGAACTTTCTGTACATCAACAGAAACAAAGCAACCAATGGAGGATT	1080
Qy	1081	TAAATTTCACTGTGGCAGTGTGATCACTCAGCGCTACCTATCTTCTGTTCTAGCCCAAGA	1140
Db	1081	TAAATTTCACTGTGGCAGTGTGATCACTCAGCGCTACCTATCTTCTGTTCTAGCCCAAGA	1140
Qy	1141	AGGCTCGGGGAAAACACAGTTTCGTTTAAAGGCTTTCTTTCTCTGTGGCAACGCCAGTG	1200
Db	1141	AGGCTCGGGGAAAACACAGTTTCGTTTAAAGGCTTTCTTTCTCTGTGGCAACGCCAGTG	1200
Qy	1201	CTACCCCATTCACAGACATCAAGTCAAATTAATTCGAGTCTGGAAAGATGTGACCCCAAGTG	1260
Db	1201	CTACCCCATTCACAGACATCAAGTCAAATTAATTCGAGTCTGGAAAGATGTGACCCCAAGTG	1260
Qy	1261	ATAAAATTTATGTGGCGGATTAATAGACTATGATTTGGTGTGAAGATGATTTATCAACAG	1320
Db	1261	ATAAAATTTATGTGGCGGATTAATAGACTATGATTTGGTGTGAAGATGATTTATCAACAG	1320
Qy	1321	GTGCTGTACTCTCCCGCAACATCAAGTTTACCAAGTACTGGACAGAAATCAAAATGGGGTGG	1380
Db	1321	GTGCTGTACTCTCCCGCAACATCAAGTTTACCAAGTACTGGACAGAAATCAAAATGGGGTGG	1380
Qy	1381	AATCTAAATCAATTAACCTCCAGCCTTATGCAGAACCTTGCAAAATAAATTAAGAACCAAG	1440
Db	1381	AATCTAAATCAATTAACCTCCAGCCTTATGCAGAACCTTGCAAAATAAATTAAGAACCAAG	1440
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Qy	1501	CAAGAAGCTCCAGTTTAAATAAGAAACAGCATTAAGAGAGAAATCTCACTACGCCAAATCGTT	1560
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Qy	1561	ACACTACACCTCAAAGCTAGAAACAGTGCCTGAAAGAAATCTCAAATTAATAATACCAAG	1620
Db	1561	ACACTACACCTCAAAGCTAGAAACAGTGCCTGAAAGAAATCTCAAATTAATAATACCAAG	1620

QY	1621	TAAATTTCAA	CAGGAAACAGACA	CAGGTTAATATGA	CAGGTTGTCTAT	TAGCCCTGAGAGCGGTTGCC	1680
DB	1621	TAAATTTCAA	CAGGAAACAGACA	CAGGTTAATATGA	CAGGTTGTCTAT	TAGCCCTGAGAGCGGTTGCC	1680
QY	1681	GCTCAGTGGAA	TTGGATCTCAAC	CAACAGACATAT	TGGAGGAGACT	TCCAAAAGAAAGGAGG	1740
DB	1681	GCTCAGTGGAA	TTGGATCTCAAC	CAACAGACATAT	TGGAGGAGACT	TCCAAAAGAAAGGAGG	1740
QY	1741	CCAAAGTGT	TTGGAGGCTTTGAA	AGGGGGTTGGAT	AAGGTTATCAT	CTGTGCTCAACAGGA	1800
DB	1741	CCAAAGTGT	TTGGAGGCTTTGAA	AGGGGGTTGGAT	AAGGTTATCAT	CTGTGCTCAACAGGA	1800
QY	1801	GCAAAAGAA	GGGGTTCTGCC	CAGAGAGAGGGGCC	CAGAGAGACT	TAAAGCTTCACTATAATGTGA	1860
DB	1801	GCAAAAGAA	GGGGTTCTGCC	CAGAGAGAGGGGCC	CAGAGAGACT	TAAAGCTTCACTATAATGTGA	1860
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DB	1921	AGAGCATGT	TGACTTTTGTA	CAAAAGGGTTATACA	CTGAAGTGTCAAA	CACAGTCAAGATT	1980
QY	1981	TTGGGAA	AGTGAACAAT	TTGAAATAGAA	GTGTGCCACAGCTT	CAAAAACCCGATGTGG	2040
DB	1981	TTGGGAA	AGTGAACAAT	TTGAAATAGAA	GTGTGCCACAGCTT	CAAAAACCCGATGTGG	2040
QY	2041	TGGGTTAT	CAGAGGCGAGCGGCTT	AAGGGCGATGCCT	TGGGTTTACAA	AAGATAGTGCGAAG	2100
DB	2041	TGGGTTAT	CAGAGGCGAGCGGCTT	AAGGGCGATGCCT	TGGGTTTACAA	AAGATAGTGCGAAG	2100
QY	2101	ACATCCT	TACTAGCTGCAAGGTAT	AATTGATGATTTCTT	CCATCCCTCCGCGATGAGTGTG	2160	
DB	2101	ACATCCT	TACTAGCTGCAAGGTAT	AATTGATGATTTCTT	CCATCCCTCCGCGATGAGTGTG	2160	
QY	2161	GGTGTGATA	CAGGCTACATA	AAGACTGTTATGAT	TCGCTTTGAA	TTTAAAGTTCATTGGAA	2220
DB	2161	GGTGTGATA	CAGGCTACATA	AAGACTGTTATGAT	TCGCTTTGAA	TTTAAAGTTCATTGGAA	2220
QY	2221	CTACCACT	TGTTTCTTAA	GAGCTATCTT	TAAAGACCAATATCT	CTTTGTTTTTAAACABAA	2280
DB	2221	CTACCACT	TGTTTCTTAA	GAGCTATCTT	TAAAGACCAATATCT	CTTTGTTTTTAAACABAA	2280
QY	2281	GATATTA	TTTGTGTATGAAT	CTAAATCAAGCCCAT	CTGTCAATATGTTACTGTCTTTTT	2340	
DB	2281	GATATTA	TTTGTGTATGAAT	CTAAATCAAGCCCAT	CTGTCAATATGTTACTGTCTTTTT	2340	
QY	2341	TAAATCAT	TGTGGTTTTGTAT	TAATTAATTTGTTGA	CTTTCTTAGATTCAC	TTCCATATGTG	2400
DB	2341	TAAATCAT	TGTGGTTTTGTAT	TAATTAATTTGTTGA	CTTTCTTAGATTCAC	TTCCATATGTG	2400
QY	2401	AATGTA	AGCTCTTAACT	TATGTCTCTTTTGT	TAAATGTGTAA	TTTCTTCTCGAAAAATAAACCAT	2460
DB	2401	AATGTA	AGCTCTTAACT	TATGTCTCTTTTGT	TAAATGTGTAA	TTTCTTCTCGAAAAATAAACCAT	2460
QY	2461	TTGTGA	ATAT	2470			
DB	2461	TTGTGA	ATAT	2470			

RESULT 14

RESOL 14
US-10-770-726-23

US-10-770-728-23
; Sequence 23, Application US/10770726

; sequence 23, Application 03/107
; Publication No. US20050266409A1

; GENERAL INFORMATION:

; GENERAL INFORMATION
; APPLICANT: Wveth

APPLICANT: Brown, Eugene

; AFFILIANT: BLOW, D
; AFFILIANT: Liu, Wei
; AFFILIANT: Liu, Wei

; TITLE OF INVENTION: COMPOSIT

; TITLE OF INVENTION: CANCERS
; TITLE OF INVENTION: CANCERS

FILE REFERENCE: AM101079 (031896-010000)

; FILE REFERENCE: AM101079 (031898-010000)
: CURRENT APPLICATION NUMBER: US/10/770.726

; CURRENT FILING DATE: 2004-02-04									
; NUMBER OF SEQ ID NOS: 48640									
; SOFTWARE: PatentIn version 3.2									
; SEQ ID NO 23									
; LENGTH: 2470									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-10-770-726-23									
Query Match 100.0%; Score 2470; DB 10; Length 2470;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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QY	61	GC CGCGTCTCTCAGGACAGCAGGCCCTCTCTCTCTGTCGGCGCGCTCAGCGTGCCC	120						
DB	61	GC CGCGTCTCTCAGGACAGCAGGCCCTCTCTCTCTGTCGGCGCGCTCAGCGTGCCC	120						
QY	121	TCGCGCCCTCAGTCTCTTTCTTAATTCBAATAAACTTGCACAGAGGACTATGAAAGATT	180						
DB	121	TCGCGCCCTCAGTCTCTTTCTTAATTCBAATAAACTTGCACAGAGGACTATGAAAGATT	180						
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QY	241	AGGTCAAACTTGGCTGCGCATATCTTACTGAGAGAGTGGTAGCTATAAAATCATGGATA	300						
DB	241	AGGTCAAACTTGGCTGCGCATATCTTACTGAGAGAGTGGTAGCTATAAAATCATGGATA	300						
QY	301	AAAACACACTAGGAGTGAATTGCGCCGGATCAAAACGGAGATTGAGGCCCTTGAAGACC	360						
DB	301	AAAACACACTAGGAGTGAATTGCGCCGGATCAAAACGGAGATTGAGGCCCTTGAAGACC	360						
QY	361	TGAGACATCAGCATATATGTCAACTCTACCATGCTTAGAGACAGCCCAAAATATTCA	420						
DB	361	TGAGACATCAGCATATATGTCAACTCTACCATGCTTAGAGACAGCCCAAAATATTCA	420						
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DB	421	TGGTCTTTGAGTACTGCCCTGGAGGAGAGCTGTTTGAATATAATTTCCAGGATCGCC	480						
QY	481	TGTCAGAAAGAGAGACCCGGGTTGCTTCGTCAGATAGTATCTGCTGTTTATGTGC	540						
DB	481	TGTCAGAAAGAGAGACCCGGGTTGCTTCGTCAGATAGTATCTGCTGTTTATGTGC	540						
QY	541	ACAGCCAGGGCTATGCTCAGGGACCTCAAGCCAGAAAATTTGCTGTTGATGAATATC	600						
DB	541	ACAGCCAGGGCTATGCTCAGGGACCTCAAGCCAGAAAATTTGCTGTTGATGAATATC	600						
QY	601	ATAAATTAAGCTGATTGACTTTTGGTCTCTGTGCAAAACCCAAAGGGTAAACAAGATTACC	660						
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QY	661	ATCTACAGACATGCTGGAGGCTGCTTATGTCAGCACTGAGTTAATCAAGAGCAAT	720						
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QY	1081	TAATTTCACTGTGGCAGTATGATCACCTCACGGCTACCTATCTTCTGCTTCTAGCCAAGA	1140						
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DB	1201	CTACCCCATTCACAGACATCAAGTCAAATTAATTTGGAGTCTGGAAGATGTGACCGCAAGTG	1260						
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DB	1321	GTGCTGCTACTCCCGAACATCAGTATTACCAAGTACTGGACAGAAATCAATGGGGTGG	1380						
QY	1381	AATCTAAATCATTTAACTCCAGCCTTATGACAGAACCTGCAAAATAAATTAAGAACAAAG	1440						
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QY	1561	ACACTACACCTCAAAAGCTAGAAAACAGTCCCTGAAAGAAAATCCAAATTAATAACAG	1620						
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DB	1621	TAAATTCACAGGAAACAGAAATTAATGACAGGTGTCAATTAGCCCTGAGAGCGGTGCC	1680						
QY	1681	GCTCAGTGAATTTGGATCTCAACCAAGCATATGAGAGAGACTCCAAAAGAAAGAGGAG	1740						
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QY	1741	CAAAAGTGTGAGGAGCTTTGAAAGGGGTGTGATAAAGTTATCACTGTGCTCACCAAGGA	1800						
DB	1741	CAAAAGTGTGAGGAGCTTTGAAAGGGGTGTGATAAAGTTATCACTGTGCTCACCAAGGA	1800						
QY	1801	GCAAAAGGAGGGTCTTCGCAGAGACGGGCCCAAGAGACTTAAAGCTTCACTATAATGTGA	1860						
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QY	1861	CTACAACTAGATTAGTGAATCCAGATCAACTGTTGAATGAATTAATGTTCTTCTTCCAA	1920						
DB	1861	CTACAACTAGATTAGTGAATCCAGATCAACTGTTGAATGAATTAATGTTCTTCTTCCAA	1920						
QY	1921	AGAAGCATGTTGATCTTTGTACAAAAGGGTTATACACTGGAAGTGTCAAAACACAGTCAAGTT	1980						
DB	1921	AGAAGCATGTTGATCTTTGTACAAAAGGGTTATACACTGGAAGTGTCAAAACACAGTCAAGTT	1980						
QY	1981	TTGGGAAAGTGACAAATTCGCAATTTGAATTTGAAGTGTGCCAGCTTCAAAAACCCGATGTGG	2040						

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2006, 19:43:24 ; Search time 560 Seconds
(without alignments)

8770.613 Million cell updates/sec

Title: US-10-656-598-1

Perfect score: 2470

Sequence: 1 ttggcgggcggaagcgcca.....ataaacatttgaatat 2470

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2477703 seqs, 994239549 residues

Total number of hits satisfying chosen parameters: 4955406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 10: /EMC_Celerra_SID33/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	937	37.9	1000	8	US-11-266-748A-222300 Sequence 222300,
2	937	37.9	1000	8	US-11-266-748A-228390 Sequence 228390,
3	937	37.9	1000	8	US-11-266-748A-339819 Sequence 339819,
4	937	37.9	1000	8	US-11-266-748A-392555 Sequence 392555,
5	937	37.9	1000	8	US-11-266-748A-470301 Sequence 470301,
6	901.6	36.5	926	8	US-11-266-748A-189434 Sequence 189434,
7	901.6	36.5	926	8	US-11-266-748A-194943 Sequence 194943,
8	791.2	32.0	1050	8	US-11-266-748A-262797 Sequence 262797,
9	791.2	32.0	1050	8	US-11-266-748A-323314 Sequence 323314,
10	717.6	29.1	758	8	US-11-266-748A-9105 Sequence 9105, Ap
11	685.4	27.7	948	8	US-11-266-748A-189435 Sequence 189435,
12	685.4	27.7	948	8	US-11-266-748A-194944 Sequence 194944,
13	590.6	23.9	728	8	US-11-266-748A-189433 Sequence 189433,
14	514	20.8	514	8	US-11-266-748A-44240 Sequence 44240, A
15	208.4	8.4	1863	9	US-11-145-471-52 Sequence 52, Appl
16	206.8	8.4	5093	8	US-11-266-748A-29698 Sequence 29698, A
17	202.4	8.2	2213	6	US-10-449-902-25149 Sequence 25149, A
18	202.4	8.2	2246	6	US-10-449-902-22550 Sequence 22550, A
19	197.8	8.0	2089	9	US-11-056-355B-48678 Sequence 48678, A
20	197.8	8.0	2089	9	US-11-056-355B-49794 Sequence 49794, A
21	196	7.9	2927	6	US-10-449-902-18825 Sequence 18825, A
22	192.8	7.8	2476	9	US-11-218-305-16612 Sequence 16612, A
23	192.6	7.8	1326	7	US-11-299-286-72 Sequence 72, Appl

24	192.6	7.8	1569	9	US-11-056-355B-89480	Sequence 89480, A	
25	192.6	7.8	1569	9	US-11-056-355B-93236	Sequence 93236, A	
26	192.6	7.8	1585	9	US-11-056-355B-47225	Sequence 47225, A	
27	192.6	7.8	1724	9	US-11-056-355B-89484	Sequence 89484, A	
28	192.6	7.8	1724	9	US-11-056-355B-93240	Sequence 93240, A	
29	190	7.7	809	8	US-11-266-748A-14709	Sequence 14709, A	
30	187.6	7.6	1229	9	US-11-056-355B-18719	Sequence 18719, A	
31	187.6	7.6	2126	9	US-11-218-305-3767	Sequence 3767, Ap	
32	186	7.5	1990	6	US-10-953-349-10926	Sequence 10926, A	
33	184.8	7.5	1539	7	US-11-299-286-2657	Sequence 2657, Ap	
34	182.8	7.4	2043	9	US-11-218-305-3768	Sequence 3768, Ap	
35	182	7.4	1909	6	US-10-953-349-25259	Sequence 25259, A	
36	182	7.4	1909	9	US-11-056-355B-67583	Sequence 67583, A	
c	37	182	7.4	2073	9	US-11-218-305-24784	Sequence 24784, A
38	180.8	7.3	2108	6	US-10-449-902-22705	Sequence 22705, A	
39	179	7.2	2017	6	US-10-612-783-997	Sequence 997, App	
40	178.8	7.2	1642	8	US-11-266-748A-252242	Sequence 252242,	
41	178.8	7.2	1642	8	US-11-266-748A-275764	Sequence 275764,	
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43	178.4	7.2	1143	8	US-11-216-545-7035	Sequence 7035, Ap	
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ALIGNMENTS

RESULT 1
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; Sequence 222300, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 222300
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-222300

Query Match 37.9%; Score 937; DB 8; Length 1000;
Best Local Similarity 100.0%; Pred. No. 2.6e-236;
Matches 937; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1654 GTGTCTATTAGCCCTGAGAGCGGTGCGCTCAGTGAATTTGGAATCTCAACAGACATA 1713
Db 121 GTGTCTATTAGCCCTGAGAGCGGTGCGCTCAGTGAATTTGGAATCTCAACAGACATA 180
Qy 1714 TGAAGAGACTCCAAAGAAAGAGGAGCCAAAGTGTGTTGGAGCCCTTGAAGGGGGTTGG 1773
Db 181 TGAAGAGACTCCAAAGAAAGAGGAGCCAAAGTGTGTTGGAGCCCTTGAAGGGGGTTGG 240
Qy 1774 ATAAGGTTATCACTGTGCTCACAGAGCAAAAGAGGTTCTGCCAGAGACGGGCCCA 1833
Db 241 ATAAGGTTATCACTGTGCTCACAGAGCAAAAGAGGTTCTGCCAGAGACGGGCCCA 300
Qy 1834 GAGACTTAAGCTTCACTAATAGTGAATCACTAAGTGAATAGTGAATCACTGTT 1893
Db 301 GAGACTTAAGCTTCACTAATAGTGAATCACTAAGTGAATAGTGAATCACTGTT 360
Qy 1894 TGAATGAATAATGTCTATTCTTCCAAAGAGCATGTTGACTTTGTACAAAAGGGTTATA 1953
Db 361 TGAATGAATAATGTCTATTCTTCCAAAGAGCATGTTGACTTTGTACAAAAGGGTTATA 420
Qy 1954 CACTGAAGTGTCAAAACACAGTCAAGATTTTGGAAAGTGACAATGCAATTTGAATTAAG 2013
Db 421 CACTGAAGTGTCAAAACACAGTCAAGATTTTGGAAAGTGACAATGCAATTTGAATTAAG 480
Qy 2014 TGTGCCAGCTTCAAAAACCCGATGTGTGGGTATCAGGAGGCGCGCTTAAGGGCGATG 2073
Db 481 TGTGCCAGCTTCAAAAACCCGATGTGTGGGTATCAGGAGGCGCGCTTAAGGGCGATG 540
Qy 2074 CCTGGGTTTCAAAAAGATTAGTGAAGACATCTCTAGCTGCAAGGTATAATTGATGG 2133
Db 541 CCTGGGTTTCAAAAAGATTAGTGAAGACATCTCTAGCTGCAAGGTATAATTGATGG 600
Qy 2134 ATTCTTCCATCCTGCCGGATGAGTGTGGGTGTGATACAGCCTACATAAAGACTGTTATGA 2193
Db 601 ATTCTTCCATCCTGCCGGATGAGTGTGGGTGTGATACAGCCTACATAAAGACTGTTATGA 660
Qy 2194 TCGCTTTGATTTTAAAGTTCAATGGAACTACCAACTTGTGTTCTTAAAGAGCTATCTTAAGA 2253
Db 661 TCGCTTTGATTTTAAAGTTCAATGGAACTACCAACTTGTGTTCTTAAAGAGCTATCTTAAGA 720
Qy 2254 CCAATATCTCTTGTGTTTAAACAAAAGATATTATTGTTGTATGAATCTAAATCAAGCC 2313
Db 721 CCAATATCTCTTGTGTTTAAACAAAAGATATTATTGTTGTATGAATCTAAATCAAGCC 780
Qy 2314 CATCTGTCAATATGTTACTGTCTTTTAAATCAATGAGTGTGTTGTATTAATTAATTGTTG 2373
Db 781 CATCTGTCAATATGTTACTGTCTTTTAAATCAATGAGTGTGTTGTATTAATTAATTGTTG 840
Qy 2374 ACTTCTTAGATTCACCTCCATATGTAATGTAAGCTCTTAACCTATGCTCTTTGTAATG 2433
Db 841 ACTTCTTAGATTCACCTCCATATGTAATGTAAGCTCTTAACCTATGCTCTTTGTAATG 900
Qy 2434 TGTAAATTTCTTCTGAAATTAACCAATTTGTGAATAT 2470
Db 901 TGTAAATTTCTTCTGAAATTAACCAATTTGTGAATAT 937

RESULT 2
US-11-266-748A-288390
; Sequence 288390, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03

; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 288390
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-288390

Query Match 37.9%; Score 937; DB 8; Length 1000;
Best Local Similarity 100.0%; Pred. No. 2.6e-236;
Matches 937; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1534 GAGAAATACCTCACTAGCCCAATCGTTACACTACACCCCTCAAAAGCTAGAAACCACTGCC 1593
Db 1 GAGAAATACCTCACTAGCCCAATCGTTACACTACACCCCTCAAAAGCTAGAAACCACTGCC 60
Qy 1594 TGAAGAAATCCCAATTAATAATACCAAGTAAATTTCAACAGGAACAGACAAATTAATGACAG 1653
Db 61 TGAAGAAATCCCAATTAATAATACCAAGTAAATTTCAACAGGAACAGACAAATTAATGACAG 120
Qy 1654 GTGTCTATTAGCCCTGAGAGCGGTGCGCTCAGTGAATTTGGAATCTCAACAGACATA 1713
Db 121 GTGTCTATTAGCCCTGAGAGCGGTGCGCTCAGTGAATTTGGAATCTCAACAGACATA 180
Qy 1714 TGAAGAGACTCCAAAGAAAGAGGAGCCAAAGTGTGTTGGAGCCCTTGAAGGGGGTTGG 1773
Db 181 TGAAGAGACTCCAAAGAAAGAGGAGCCAAAGTGTGTTGGAGCCCTTGAAGGGGGTTGG 240
Qy 1774 ATAAGGTTATCACTGTGCTCACAGAGCAAAAGAGGTTCTGCCAGAGACGGGCCCA 1833
Db 241 ATAAGGTTATCACTGTGCTCACAGAGCAAAAGAGGTTCTGCCAGAGACGGGCCCA 300
Qy 1834 GAGACTTAAGCTTCACTAATAGTGAATCACTAAGTGAATAGTGAATCACTGTT 1893
Db 301 GAGACTTAAGCTTCACTAATAGTGAATCACTAAGTGAATAGTGAATCACTGTT 360
Qy 1894 TGAATGAATAATGTCTATTCTTCCAAAGAGCATGTTGACTTTGTACAAAAGGGTTATA 1953
Db 361 TGAATGAATAATGTCTATTCTTCCAAAGAGCATGTTGACTTTGTACAAAAGGGTTATA 420
Qy 1954 CACTGAAGTGTCAAAACACAGTCAAGATTTTGGAAAGTGACAATGCAATTTGAATTAAG 2013
Db 421 CACTGAAGTGTCAAAACACAGTCAAGATTTTGGAAAGTGACAATGCAATTTGAATTAAG 480
Qy 2014 TGTGCCAGCTTCAAAAACCCGATGTGTGGGTATCAGGAGGCGCGCTTAAGGGCGATG 2073
Db 481 TGTGCCAGCTTCAAAAACCCGATGTGTGGGTATCAGGAGGCGCGCTTAAGGGCGATG 540
Qy 2074 CCTGGGTTTCAAAAAGATTAGTGAAGACATCTCTAGCTGCAAGGTATAATTGATGG 2133
Db 541 CCTGGGTTTCAAAAAGATTAGTGAAGACATCTCTAGCTGCAAGGTATAATTGATGG 600
Qy 2134 ATTCTTCCATCCTGCCGGATGAGTGTGGGTGTGATACAGCCTACATAAAGACTGTTATGA 2193
Db 601 ATTCTTCCATCCTGCCGGATGAGTGTGGGTGTGATACAGCCTACATAAAGACTGTTATGA 660
Qy 2194 TCGCTTTGATTTTAAAGTTCAATGGAACTACCAACTTGTGTTCTTAAAGAGCTATCTTAAGA 2253


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; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 399255
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-399255

Query Match      37.9%; Score 937; DB 8; Length 1000;
Best Local Similarity 100.0%; Pred. No. 2.6e-236;
Matches 937; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1534 GAGAAATACCTACAGCCCAATCGTTACACTACACCCCTCAAAAGCTAGAAACCAAGTGC 1593
Db 1 GAGAAATACCTACAGCCCAATCGTTACACTACACCCCTCAAAAGCTAGAAACCAAGTGC 60

Qy 1594 TGAAGAAACTCCAATTAAATACCAAGTAAATCAACAGGAACAGACAAAGTTAATGACAG 1653
Db 61 TGAAGAAACTCCAATTAAATACCAAGTAAATCAACAGGAACAGACAAAGTTAATGACAG 120

Qy 1654 GTGTCTATTAGCCCTGAGAGCGGTGCGCTCAGTGGAAATGGATCTCAACCAAGACACATA 1713
Db 121 GTGTCTATTAGCCCTGAGAGCGGTGCGCTCAGTGGAAATGGATCTCAACCAAGACACATA 180

Qy 1714 TGAAGAGACTCCAAAAGAAAGGAGCCCAAGTGTGGAGCCCTTGAAGGGGGTGG 1773
Db 181 TGAAGAGACTCCAAAAGAAAGGAGCCCAAGTGTGGAGCCCTTGAAGGGGGTGG 240

Qy 1774 ATAAGGTTATCACTGTGCTCACCAGAGCAAAAGAGGGTCTGCCAGAGCGGCCCA 1833
Db 241 ATAAGGTTATCACTGTGCTCACCAGAGCAAAAGAGGGTCTGCCAGAGCGGCCCA 300

Qy 1834 GAAGACTAAAGCTTCACTATAATGTGACTAACAATAGTGAATTCAGATCAACTGT 1893
Db 301 GAAGACTAAAGCTTCACTATAATGTGACTAACAATAGTGAATTCAGATCAACTGT 360

Qy 1894 TGAATGAATAATGTCTATTCTTCCAAAGAGCATGTGACTTTGTACAAAAGGGTTATA 1953
Db 361 TGAATGAATAATGTCTATTCTTCCAAAGAGCATGTGACTTTGTACAAAAGGGTTATA 420

Qy 1954 CACTGAAGTGTCAAAACACAGTCAGATTTGGGAAAGTGACAAATGCAATTTGAATTAGAAG 2013
Db 421 CACTGAAGTGTCAAAACACAGTCAGATTTGGGAAAGTGACAAATGCAATTTGAATTAGAAG 480

Qy 2014 TGTGCCAGCTTCAAAAACCCGATGTGGTGGTATCAGAGGCGACGGCTTAAAGGGCGATG 2073
Db 481 TGTGCCAGCTTCAAAAACCCGATGTGGTGGTATCAGAGGCGACGGCTTAAAGGGCGATG 540

Qy 2074 CTTGGGTTTCAAAAGNTTGTGGAGACATCTCTATCTAGCTGCAAGGTATATTGATGG 2133
Db 541 CTTGGGTTTCAAAAGNTTGTGGAGACATCTCTATCTAGCTGCAAGGTATATTGATGG 600

Qy 2134 ATTCTTCCATCTCCCGGATGAGTGTGGGTGTGATACAGCTCATATAAGACTGTTATGA 2193
Db 601 ATTCTTCCATCTCCCGGATGAGTGTGGGTGTGATACAGCTCATATAAGACTGTTATGA 660

Qy 2194 TCGCTTTGATTTTAAAGTTCAITGGAACTACCAACTTGTGTTTCTAAAGAGCTATCTTAA 2253
Db 661 TCGCTTTGATTTTAAAGTTCAITGGAACTACCAACTTGTGTTTCTAAAGAGCTATCTTAA 720

Qy 2254 CCAATATCTCTTTGTTTTTAAACAAAGATATTTATTTGTGTATGAATCTTAAATCAAGCC 2313
Db 721 CCAATATCTCTTTGTTTTTAAACAAAGATATTTATTTGTGTATGAATCTTAAATCAAGCC 780
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2314 CATCTGTCATTAAGTATCTGCTCTTTTAAATCATGTGGTTTTGTATATAATTAATAATTGTTG 2373
Db 781 CATCTGTCATTAAGTATCTGCTCTTTTAAATCATGTGGTTTTGTATATAATTAATAATTGTTG 840

Qy 2374 ACTTTCTTAGATTCACCTTCCATATGGAATGTAAGCTCTTAACTATGTCTCTTTGTAATG 2433
Db 841 ACTTTCTTAGATTCACCTTCCATATGGAATGTAAGCTCTTAACTATGTCTCTTTGTAATG 900

Qy 2434 TGTAAATTTCTTTCTGAAATATAAACCAATTTGTGAATAT 2470
Db 901 TGTAAATTTCTTTCTGAAATATAAACCAATTTGTGAATAT 937

RESULT 5
US-11-266-748A-470301/c
; Sequence 470301, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 470301
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-470301

Query Match      37.9%; Score 937; DB 8; Length 1000;
Best Local Similarity 100.0%; Pred. No. 2.6e-236;
Matches 937; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1534 GAGAAATACCTACAGCCCAATCGTTTACACTACACCCCTCAAAAGCTAGAAACCAAGTGC 1593
Db 1000 GAGAAATACCTACAGCCCAATCGTTTACACTACACCCCTCAAAAGCTAGAAACCAAGTGC 941

Qy 1594 TGAAGAAACTCCAATTAAATACCAAGTAAATCAACAGGAACAGACAAAGTTAATGACAG 1653
Db 940 TGAAGAAACTCCAATTAAATACCAAGTAAATCAACAGGAACAGACAAAGTTAATGACAG 881

Qy 1654 GTGTCTATTAGCCCTGAGAGCGGTGCGCTCAGTGGAAATTTGGATCTCAACCAAGACACATA 1713
Db 880 GTGTCTATTAGCCCTGAGAGCGGTGCGCTCAGTGGAAATTTGGATCTCAACCAAGACACATA 821

Qy 1714 TGAAGAGACTCCAAAAGAAAGGAGCCCAAGTGTGGAGCCCTTGAAGGGGGTGG 1773
Db 820 TGAAGAGACTCCAAAAGAAAGGAGCCCAAGTGTGGAGCCCTTGAAGGGGGTGG 761

Qy 1774 ATAAGGTTATCACTGTGCTCACCAGAGCAAAAGAGGGTCTTGCAGAGAGCGGCCCA 1833
Db 760 ATAAGGTTATCACTGTGCTCACCAGAGCAAAAGAGGGTCTTGCAGAGAGCGGCCCA 701
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QY 1834 GAAGACTAAAGCTTCACTAATAATGTGACTACAACTAGATTAGTGAATCCAGATCAACTGT 1893
DB 700 GAAGACTAAAGCTTCACTAATAATGTGACTACAACTAGATTAGTGAATCCAGATCAACTGT 641
QY 1894 TGAATGAAATAATGTCTATTCTTCCAAAGAACGATGTTGACTTTGTACAAAAGGGTTATA 1953
DB 640 TGAATGAAATAATGTCTATTCTTCCAAAGAACGATGTTGACTTTGTACAAAAGGGTTATA 581
QY 1954 CACTGAAGTGTCAAAACACAGTCAAGATTTTGGGAAAGTGAACAATGCAATTTGAATTAGAAG 2013
DB 580 CACTGAAGTGTCAAAACACAGTCAAGATTTTGGGAAAGTGAACAATGCAATTTGAATTAGAAG 521
QY 2014 TGTGCCAGCTTCAAAAACCGATGTGGTGGGTATCAGAGGCGACGGCTTAAGGGCGATG 2073
DB 520 TGTGCCAGCTTCAAAAACCGATGTGGTGGGTATCAGAGGCGACGGCTTAAGGGCGATG 461
QY 2074 CTTGGGGTTTACAAAAGATTAGTGGAAAGACATCTCTATCTAGCTCAAGGTATTAATTCATGG 2133
DB 460 CTTGGGGTTTACAAAAGATTAGTGGAAAGACATCTCTATCTAGCTCAAGGTATTAATTCATGG 401
QY 2134 ATTCTTCCATCTCCGCGATGAGTGTGGGTGATACAGCTACATAAAAGACTGTTTATGA 2193
DB 400 ATTCTTCCATCTCCGCGATGAGTGTGGGTGATACAGCTACATAAAAGACTGTTTATGA 341
QY 2194 TGCCTTTGATTTAAAGTTCATTGGAACTACCAACTTGTTCCTTAAAGAGCTATCTTAAGA 2253
DB 340 TGCCTTTGATTTAAAGTTCATTGGAACTACCAACTTGTTCCTTAAAGAGCTATCTTAAGA 281
QY 2254 CCAATATCTCTTGTGTTTAAACAAAGATATTTATTTGTGTATGAATCTTAATCAAGCC 2313
DB 280 CCAATATCTCTTGTGTTTAAACAAAGATATTTATTTGTGTATGAATCTTAATCAAGCC 221
QY 2314 CATCTGTCAATTATGTTACTGTCTTTTAAATCAATGTGGTTTGTATTAATTAATTTGTTG 2373
DB 220 CATCTGTCAATTATGTTACTGTCTTTTAAATCAATGTGGTTTGTATTAATTAATTTGTTG 161
QY 2374 ACTTCTTAGATTCACCTCCATATGAAATGAACTCTTAATGCTTTAATGCTCTTTTGAATG 2433
DB 160 ACTTCTTAGATTCACCTCCATATGAAATGAACTCTTAATGCTCTTTAATGCTCTTTTGAATG 101
QY 2434 TGTAAATTTCTTCTGAAATTAACCAATTTGTGATAT 2470
DB 100 TGTAAATTTCTTCTGAAATTAACCAATTTGTGATAT 64

RESULT 6

US-11-266-748A-189434
; Sequence 189434, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnstone, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662, 276
; PRIOR FILING DATE: 2005-03-14

; PRIOR APPLICATION NUMBER: US 60/700, 293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 189434
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-189434

Query Match 36.5%; Score 901.6; DB 8; Length 926;
Best Local Similarity 99.5%; Pred. No. 5.1e-227;
Matches 915; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 33 CGAAAGATTTCTTAGGAACGCGGTACAGCCGCTCTCTCAGGACAGAGGCGCCCTGTCC 92
DB 5 CGAAAGATTTCTTAGGAACGCGGTACAGCCGCTCTCTCAGGACAGAGGCGCCCTGTCC 64
QY 93 TTCTGTGGGCGCGCTCAGCCGTGCGCTCCGCGCTCTCAGGTTCTTTTCTTAATTCAAA 152
DB 65 TTCTGTGGGCGCGCTCAGCCGTGCGCTCCGCGCTCTCAGGTTCTTTTCTTAATTCAAA 124
QY 153 TAAACTTGCACAGAGGACTATGAAGATTATGATGAACCTTCTCAAAATATTATGAATTCACAT 212
DB 125 TAAACTTGCACAGAGGACTATGAAGATTATGATGAACCTTCTCAAAATATTATGAATTCACAT 184
QY 213 GAAACTATTGGGACAGGTGGCTTTTGCAGAGGTCAAACTTGGCCTGCCATATCTTACTGGA 272
DB 185 GAAACTATTGGGACAGGTGGCTTTTGCAGAGGTCAAACTTGGCCTGCCATATCTTACTGGA 244
QY 273 GAGATGTAGCTATAAAATCATGGATAAAACACACATAGGAGTGAATTTGCCCGGATC 332
DB 245 GAGATGTAGCTATAAAATCATGGATAAAACACACATAGGAGTGAATTTGCCCGGATC 304
QY 333 AAAACGAGATTTGAGGCTTTGAAGAACCTTGAGACATATGTCACATATATGTCACCTACCAT 392
DB 305 AAAACGAGATTTGAGGCTTTGAAGAACCTTGAGACATATGTCACATATATGTCACCTACCAT 364
QY 393 GTGCTAGAGACAGCCAAACAAATATTTCATGGTTCTTGAGTACTGCGCTGGAGGAGCTG 452
DB 365 GTGCTAGAGACAGCCAAACAAATATTTCATGGTTCTTGAGTACTGCGCTGGAGGAGCTG 424
QY 453 TTTGACTATATAATTTCCAGGATCGCTGTGAGAGGAGAACCCGGGTGTCTTCCGT 512
DB 425 TTTGACTATATAATTTCCAGGATCGCTGTGAGAGGAGAACCCGGGTGTCTTCCGT 484
QY 513 CAGATAGTATCTGCTGTTGCTTATGTCACAGCCAGGGCTATGCTCACAGGACCTCAAG 572
DB 485 CAGATAGTATCTGCTGTTGCTTATGTCACAGCCAGGGCTATGCTCACAGGACCTCAAG 544
QY 573 CCAGAAAATTTGCTGTTGATGAATATATAAATTTAAAGCTGATGACTTTGGTCTCTGT 632
DB 545 CCAGAAAATTTGCTGTTGATGAATATATAAATTTAAAGCTGATGACTTTGGTCTCTGT 604
QY 633 GCAAAACCAAGGGTAAACAAGGATTAACATCTACAGACATGCTGTGGGAGTCTGGCTTAT 692
DB 605 GCAAAACCAAGGGTAAACAAGGATTAACATCTACAGACATGCTGTGGGAGTCTGGCTTAT 664
QY 693 GCAGCACCTGAGTTAATACAGGCAATCATATCTTGGATCAGAGGAGATGTTGGAGC 752
DB 665 GCAGCACCTGAGTTAATACAGGCAATCATATCTTGGATCAGAGGAGATGTTGGAGC 724
QY 753 ATGGGCATACCTGTTATATGTTCTTATGTTGATTTTACACATTTGATGATGATATGTA 812
DB 725 ATGGGCATACCTGTTATATGTTCTTATGTTGATTTTCTACCATTTGATGATGATATGTA 784
QY 813 ATGGCTTTTATCAAGAGATTATGAGAGAAATATGATGTTTCCCAAGTGGCTCTCTCCC 872
DB 785 ATGGCTTTTATCAAGAGATTATGAGAGAAATATGATGTTTCCCAAGTGGCTCTCTCCC 844
QY 873 AGTAGCATTTCTCTTCTTCAAAATGCTGAGGTGGACCCCAAGAAACGATTTCTATG 932
DB 845 AGTAGCATTTCTCTTCTTCAAAATGCTGCA-GTGGACCCCAAGAAACGATTTCTATG 903

QY 933 AAAAAATCTATTGAACCATCC 952
Db 904 AAAAAATCTATTGAACCATCC 923

RESULT 7
US-11-266-748A-194943
; Sequence 194943, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662, 276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700, 293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 194943
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-194943

Query Match 36.5%; Score 901.6; DB 8; Length 926;
Best Local Similarity 99.5%; Pred. No. 5.1e-227;
Matches 915; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 33 CGAAAAAGATTCTTAGGAACGCCGTACAGCCGGTCTCTCAGGACAGCAGGCCCTGTCC 92
Db 5 CGAAAAAGATTCTTAGGAACGCCGTACAGCCGGTCTCTCAGGACAGCAGGCCCTGTCC 64

QY 93 TTCTGTGGGCGCGCTCAGCCGTGGCTCGCCCTCGCCCTCAGGTTCTTTTCTAATTCGAA 152
Db 65 TTCTGTGGGCGCGCTCAGCCGTGGCTCGCCCTCGCCCTCAGGTTCTTTTCTAATTCGAA 124

QY 153 TAAACTTGCAAGAGGACTATGAAGATTATGATGAACCTCTCAATATATGATTAATACAT 212
Db 125 TAAACTTGCAAGAGGACTATGAAGATTATGATGAACCTCTCAATATATGATTAATACAT 184

QY 213 GAAACTATTGGGACAGGTGGCTTTGCAAAAGGTCAAACTTGCCTGCCATATCCTTACTGGA 272
Db 185 GAAACTATTGGGACAGGTGGCTTTGCAAAAGGTCAAACTTGCCTGCCATATCCTTACTGGA 244

QY 273 GAGATGTAGCTATAAAATCATGATATAAAACACACTAGGAGTGAATTTGCCCGGATC 332
Db 245 GAGATGTAGCTATAAAATCATGATATAAAACACACTAGGAGTGAATTTGCCCGGATC 304

QY 333 AAAACGGAGATTGAGGCTTTGAAGAACCTCAGACATCAGCATATATGCTCAACTCTACCAT 392
Db 305 AAAACGGAGATTGAGGCTTTGAAGAACCTCAGACATCAGCATATATGCTCAACTCTACCAT 364

QY 393 GTGCTAGAGACAGCCAAACAAAATATTTCATGTTCTTGTAGTACTGCCCTGGAGAGAGCTG 452

Db 365 GTGCTAGAGACAGCCAAACAAAATATTTCATGGTTCTTGGAGTACTGCCCTGGAGAGAGCTG 424
QY 453 TTTGACTATATAATTTTCCAGGATCGCTGTGAGAGAGGAGACCCGGGTTTCTTCCCT 512
Db 425 TTTGACTATATAATTTTCCAGGATCGCTGTGAGAGAGGAGACCCGGGTTTCTTCCCT 484
QY 513 CAGATAGTATCTGCTGTTGCTTATGTGCACAGCCAGGGCTATGCTCAGAGGACCTCAAG 572
Db 485 CAGATAGTATCTGCTGTTGCTTATGTGCACAGCCAGGGCTATGCTCAGAGGACCTCAAG 544
QY 573 CCAGAAAATTTGCTGTTGATGAATATCATAAATTAAGCTGATTTGGTCTCTCT 632
Db 545 CCAGAAAATTTGCTGTTGATGAATATCATAAATTAAGCTGATTTGGTCTCTCT 604
QY 633 GCAAAACCCAGGGTAAACAAGGATTACCATCTACAGACATGCTGTGGGAGTCTGGCTTAT 692
Db 605 GCAAAACCCAGGGTAAACAAGGATTACCATCTACAGACATGCTGTGGGAGTCTGGCTTAT 664
QY 693 GCAGCACCTGAGTTAATACAGGCAAAATCATATCTTGGATCAGAGGACAGATGTTGGAGC 752
Db 665 GCAGCACCTGAGTTAATACAGGCAAAATCATATCTTGGATCAGAGGACAGATGTTGGAGC 724
QY 753 ATGGGCATCTGTTATATGTTCTTATGTGGAATTTCTACCATTTGATGATGATTAATGTA 812
Db 725 ATGGGCATCTGTTATATGTTCTTATGTGGAATTTCTACCATTTGATGATGATTAATGTA 784
QY 813 ATGGCTTTATACAGAAGATTATGAGAGGAAATATGATGTTCCCAAGTGGCTCTCTCCC 872
Db 785 ATGGCTTTATACAGAAGATTATGAGAGGAAATATGATGTTCCCAAGTGGCTCTCTCCC 844
QY 873 AGTAGCATTTCTCTTCTTCAACAAATGCTGAGGTGGAGCCCAAGAAACGGATTTCTATG 932
Db 845 AGTAGCATTTCTCTTCTTCAACAAATGCTGCA-GTGGACCCCAAGAAACGGATTTCTATG 903

QY 933 AAAAAATCTATTGAACCATCC 952
Db 904 AAAAAATCTATTGAACCATCC 923

RESULT 8
US-11-266-748A-262797
; Sequence 262797, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662, 276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700, 293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 262797
; LENGTH: 1050
; TYPE: DNA


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Db 671 TGATAAAATTAATGTGGCGGATTAATAGACTATGATTTGGTGTGAAGATGATTTATCAAC 612
Qy 1319 AGGTGCTGTACTCCCGAACATCACTAGTTTACCAAGTACTGACAGAGATCAATCAATGGGCT 1378
Db 611 AGGTGCTGTACTCCCGAACATCACTAGTTTACCAAGTACTGACAGAGATCAATCAATGGGCT 552
Qy 1379 GGAATCTAAATCAATTAATCTCCAGCTTATGACAGACACCTGCAAAATAAAATTAAGAACAA 1438
Db 551 GGAATCTAAATCAATTAATCTCCAGCTTATGACAGACACCTGCAAAATAAAATTAAGAACAA 492
Qy 1439 AGAAATGTATATATCTCTTAAGTCTGCTGTAAGAAATGAAGAGTACTTTATGTTTCTCTGA 1498
Db 491 AGAAATGTATATATCTCTTAAGTCTGCTGTAAGAAATGAAGAGTACTTTATGTTTCTCTGA 432
Qy 1499 GCCAAAGACTCCAGTTTAATGAACACAGCAGCAGTAAGAGAGAAATCTACTACGCCAATCG 1558
Db 431 GCCAAAGACTCCAGTTTAATGAACACAGCAGCAGTAAGAGAGAAATCTACTACGCCAATCG 372
Qy 1559 TTACACTACACCTCAAAAGCTAGAAACAGTGCCTGAAAGAACTCCCAATTAATAATACC 1618
Db 371 TTACACTACACCTCAAAAGCTAGAAACAGTGCCTGAAAGAACTCCCAATTAATAATACC 312
Qy 1619 AGTAAATTTCAACA-GGAACAGACAAGTTAATGACAGGTGTCAATTAG-CCCTGAGAGCGG 1676
Db 311 AGTAAATTTCAACAAGGAGCAAGCAAGTTAATGACAGGTGTCAATTAGCCCTCGAGAGCGG 252
Qy 1677 TG-CCGCTCAGTGGA--TTGGATCTCAACCAAGCAGCATAT-GGAGGAGACTCCAAAGAG 1732
Db 251 TGCCCGCTCAGTGGAAATTTGGGATCTCAACCAAGCAGCATATGGGAGGAGACTCCAAAGAG 192
Qy 1733 AAA-GGGAGCCAAAGTGT-TT-GGGAGCTTGAAGGGGGTTGG--ATAAGGTTTATCACT 1787
Db 191 AAAGGGAGCCAAAGTGT-TTGGGAGCTTGAAGGGGGTTGGAAATAGGGTTATCACT 132
Qy 1788 -GTGCTCACCAGGAGC-AAAAGGAAGGGTTCTCCACAG 1823
Db 131 GGGGCTCACCAGGAGCAAAAGGAGGGTTCTGCCAAA 94
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RESULT 10
US-11-266-748A-9105
; Sequence 9105, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 5815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9105
; LENGTH: 758
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; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (427)..(427)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-9105

Query Match 29.1%; Score 717.6; DB 8; Length 758;
Best Local Similarity 98.5%; Pred. No. 1.3e-178;
Matches 745; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

Qy 1715 GGAGGAGACTCCAAAAGAAAGGAGCCAAAGCTGTTGGAGCCTTGAAGGGGGTTGA 1774
Db 3 GCAGGAGACTCCAAAAGAAAGGAGCCAAAGCTGTTGGAGCCTTGAAGGGGGTTGA 62
Qy 1775 TAAAGTTATCACTGTGCTCACCAGGAGCAAAAGGAAGGGTTCTGCAGAGAGCGGCCAG 1834
Db 63 TAAAGTTATCACTGTGCTCACCAGGAGCAAAAGGAAGGGTTCTGCAGAGAGCGGCCAG 122
Qy 1835 AAGACTTAAAGCTTCACTATAATGTGACTACAACTAGATTAGTGAATCCAGATCAACTGTT 1894
Db 123 AAGACTTAAAGCTTCACTATAATGTGACTACAACTAGATTAGTGAATCCAGATCAACTGTT 182
Qy 1895 GAATGAAATAATGTCTATTCTTTCCAAAGAGCATGTTGACTTTGTACAAAAGGGTTATAC 1954
Db 183 GAATGAAATAATGTCTATTCTTTCCAAAGAGCATGTTGACTTTGTACAAAAGGGTTATAC 242
Qy 1955 ACTGAAGTGTCAAAACACAGTCAAGTTTGGGAAAGTGACAATGCAATTTGAATTAGAAGT 2014
Db 243 ACTGAAGTGTCAAAACACAGTCAAGTTTGGGAAAGTGACAATGCAATTTGAATTAGAAGT 302
Qy 2015 GTGCCAGCTTCAAAACCCGATGTGGGTATCAGGAGGAGCGGCTTAAAGGGCGATGC 2074
Db 303 GTGCCAGCTTCAAAACCCGATGTGGGTATCAGGAGGAGCGGCTTAAAGGGCGATGC 362
Qy 2075 CTGGGTTTACAAAAGATTAGTGGAGACATCTATCTAGCTCAAGGTATAATTTGATGGA 2134
Db 363 CTGGGTTTACAAAAGATTAGTGGAGACATCTATCTAGCTCAAGGTATAATTTGATGGA 422
Qy 2135 TTCT-TCCATCTCGCGGATGAGTGGGTGTGATACAGCCCTACATAAAGACTGTTATGA 2193
Db 423 TTCTTCCATCTCGCGGATGAGTGGGTGTGATACAGCCCTACATAAAGACTGTTATGA 482
Qy 2194 TCGCTTTGATTTTAAAGTTCAATTGGAACTACCAACTTTGTTCTTAAAGAGCTATCTTAAGA 2253
Db 483 TCGCTTTGATTTTAAAGTTCAATTGGAACTACCAACTTTGTTCTTAAAGAGCTATCTTAAGA 542
Qy 2254 CCAATATCTCTTTGTTTAAACAAAAGATATATTTTGTGTATGAATCTAAATCAAGCC 2313
Db 543 CCAATATCTCTTTGTTTAAACAAAAGATATATTTTGTGTATGAATCTAAATCAAGCC 602
Qy 2314 CATCTGTCAATATGTTACTGCTTTTAAATCATGTTGGTTTGTATATTAATTAATTTG 2373
Db 603 CATCTGTCAATATGTTACTGCTTTTAAATCATGTTGGTTTGTATATTAATTAATTTG 662
Qy 2374 ACTTTCTTAGATTCACTTCCATATGTAATGTAAGCTCTTAACT-ATGCTCTTTTGTAT 2432
Db 663 ACTTTCTTAGATTCACTTCCATATGTAATGTAAGCTCTTAACTATGCTCTTTCGAAT 722
Qy 2433 GTGTAATTTCTTTCTGAAATAAAACCAATTTGTGAAT 2468
Db 723 GTGTAATTTCTCTCTGAAATAAAACCAATTTGTGCAT 758

RESULT 11
US-11-266-748A-189435
; Sequence 189435, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
```


		Matches	696;	Conservative	0;	Mismatches	14;	Indels	87;	Gaps	1;
QY	872	CAGTAGCATTCTGCTTCTTCAACAAATGCTGAGGTGGACCCAAAGAAACGGATTTCAT									
Db	522	CAGTAGCATTCTGCTTCTTCAACAAATGCTGAGGTGGACCCAAAGAAACGGATTTCAT									
QY	932	GAAAAATCTATTGAACCATCCCTGGATCATGCAAGATTACAATATCCTGTTGAGTGGA									
Db	582	GAAAAATCTATTGAACCATCCCTGGATCATGCAAGATTACAATATCCTGTTGAGTGGA									
QY	992	AAGCAGAATCCTTTTATTCACCTCGATGATGATGCGTAAACAGAACTTCTGTACATCA									
Db	642	AAGCAGAATCCTTTTATTCACCTCGATGATGATGCGTAAACAGAACTTCTGTACATCA									
QY	1052	CAGAAACAACAGGCAACAATGAGGATTAAATTCACCTGTCAGTATGATCACCCTCAC									
Db	702	CAGAAACAACAGGCAACAATGAGGATTAAATTCACCTGTCAGTATGATCACCCTCAC									
QY	1112	GGCTACCTATCTTCTGCTTCTAGCCAAAGGCTCGGGGAAAACCAAGTTGCTTTAAGGCT									
Db	762	GGCTACCTATCTTCTGCTTCTAGCCAAAGAA-GCTCGGGGAAAACCAAGTTGCTTTAAGCT									
QY	1172	TTCTTCTTCTCTGTGGCAAGCCAGTGTACCCCAATTCACAGACATCAAGTCAATAA									
Db	821	TTCTTCTTCTCTGTGGCAAGCCAGTGTACCCCAATTCACAGACATCAAGTCAATAA									
QY	1232	TTGGAGTCTGGAAGATGTGACCCCAAGTGTATATAAAATTAATGTGGCGGATTAATAGACTA									
Db	881	TTGGAGTCTGGAAGATGTGACCCCAAGTGTATATAAAATTAATGTGGCGGATTAATAGACTA									
QY	1292	TGATTGGTG 1300									
Db	940	TGATTGGTG 948									

RESULT 14
US-11-266-748A-44240
; Sequence 44240, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2

Query Match 23.9%; Score 590.6; DB 8; Length 728;
Best Local Similarity 87.3%; Pred. No. 3.4e-145;

; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 44240
; LENGTH: 520
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-44240

Query Match 20.8%; Score 514; DB 8; Length 520;
Best Local Similarity 100.0%; Pred. No. 4.3e-125; Indels 0; Gaps 0;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1956 CTGAAGTGTCAACACAGTCAGATTTTGGGAAGTGACAAATGCAATTTGCAATTTAGAAGTG 2015
DB 1 CTGAAGTGTCAACACAGTCAGATTTTGGGAAGTGACAAATGCAATTTGCAATTTAGAAGTG 60
QY 2016 TGCAGCTTCAAAAACCCGATGTGGGTATCAGGAGCAGCGGCTTAAGGGCGATGCC 2075
DB 61 TGCAGCTTCAAAAACCCGATGTGGGTATCAGGAGCAGCGGCTTAAGGGCGATGCC 120
QY 2076 TGGTTTACAAAGATTAGTGGAGACATCCCTATCTAGCTGCAAGTATATTTGATGAT 2135
DB 121 TGGTTTACAAAGATTAGTGGAGACATCCCTATCTAGCTGCAAGTATATTTGATGAT 180
QY 2136 TCTTCATCTCTGCGGATGAGTGTGGGTGTGATACAGCCTACATAAAGACTGTTATGATC 2195
DB 181 TCTTCATCTCTGCGGATGAGTGTGGGTGTGATACAGCCTACATAAAGACTGTTATGATC 240
QY 2196 GCTTTGATTTAAAGTTTCATGGAACCTACCACTGTTTCTAAAGAGCTATCTTAAGACC 2255
DB 241 GCTTTGATTTAAAGTTTCATGGAACCTACCACTGTTTCTAAAGAGCTATCTTAAGACC 300
QY 2256 AATACTCTTTGTTTAAACAAAGATATTTTGTGTATGAATCTAAATCAAGCCCA 2315
DB 301 AATACTCTTTGTTTAAACAAAGATATTTTGTGTATGAATCTAAATCAAGCCCA 360
QY 2316 TCTGTCAATATGTTACTGTTCTTTTAAATCATGTGTTTGTATATTAATAATTTGTGAC 2375
DB 361 TCTGTCAATATGTTACTGTTCTTTTAAATCATGTGTTTGTATATTAATAATTTGTGAC 420
QY 2376 TTCTTGAATTCATCTTCCATATGTGAATGTAAGCTCTTAAGTATGCTCTTTGTAATG 2435
DB 421 TTCTTGAATTCATCTTCCATATGTGAATGTAAGCTCTTAAGTATGCTCTTTGTAATG 480
QY 2436 TAATTTCTTTCTGAATAAACCATTGTTGAATA 2469
DB 481 TAATTTCTTTCTGAATAAACCATTGTTGAATA 514

RESULT 15
US-11-145-471-52
; Sequence 52, Application US/11145471
; Publication No. US20060147947A1
; GENERAL INFORMATION:
; APPLICANT: Apfeld, Javier
; APPLICANT: O'Conner, Gregory
; TITLE OF INVENTION: AMPK Pathway Components
; FILE REFERENCE: 13407-0570011

; CURRENT APPLICATION NUMBER: US/11/145,471
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: PCT/US/2003/38628
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/430,804
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: US 60/488,261
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 60/578,804
; PRIOR FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-145-471-52

Query Match 8.4%; Score 208.4; DB 9; Length 1863;
Best Local Similarity 55.6%; Pred. No. 2.3e-44;
Matches 470; Conservative 0; Mismatches 361; Indels 15; Gaps 3;
QY 212 TGAAACTATTGGACACAGGTGGCTTTGCAAGGTCAAACTTTGCTGCCATATCTCTACTGG 271
DB 86 TGACACGCTGGGGTGGCACCCTTCGGCAAGTGAAGTTGGCAACATGAATTGACTGG 145
QY 272 AGAGATGGTAGCTATAAAATCATGATAAAACACACTAGGGAG-----TGATTTGCC 325
DB 146 GCATAAAGTAGCTGTGAAGATACTCAATCGACAGAAGATTTCGGAGCCTTGATGTGGTAGG 205
QY 326 CCGGATCAAAACGGAGATTGAGGCCCTTGGAACCTGAGACATCAGACATATATGTCAACT 385
DB 206 AAAAAATCCGACAGAAAATTCAGAACCTCAAGCTTTTCAGGCATCTCATATAATTAACCT 265
QY 386 CTACCATGTGCTAGAGACAGCCCAACAAATATTTTCATGTTCTTGAGTACTGCCCTCGAGG 445
DB 266 GTACCAAGTCACTCAGTACACCATCTGATATTTTCATGGTGATGGATATGTCTCAGGAGG 325
QY 446 AGAGCTGTTTGAATATATAATTTCCAGGATCGCCTGTGAGAGAGGACCCGGGTTGT 505
DB 326 AGAGCTATTTGATTATATCTGTAAGAAATGGAAGCTGGATGAAAGAAAGTCGGCGTCT 385
QY 506 CTTCCGTGAGATAGTATCTGCTGTTTATGTGCAAGCAGGCGGTATGCTCAGAGGA 565
DB 386 GTTCCAAACAGATCTTTCTGGTGTGGAATTAATTTGTACAGGCATATGTTGTTCCATAGAGA 445
QY 566 CTTCAAGCCAGAAAATTTGCTGTTTGTGAATATCATATAATTTAAAGCTGATTGACTTTCG 625
DB 446 TTTGAAACCTGAAAATGCTCTGTTGATGCAACATGAATGCAAAAGATAGCTGATTTTGG 505
QY 626 TCTCTGTGCAAAACCCAGGGTAAACAGGATTTACCATCTACAGACATGCTGGGAGTCT 685
DB 506 TCTTTC-----AAACATGATGTGATGGTGAATTTTAAAGCAACAGTTTGGCTCACC 559
QY 686 GGCCTATGAGCACCCTGAGTTAAATCAAGGCAAAATCATATCTTTGGATCAGAGCGAGATGT 745
DB 560 CAACTATGTGCAACAGAAATTTTCAGGAAGATTGTATGCAAGGCCACAGAGTAGATAT 619
QY 746 TTGGAGCATGGGCATCTGTTATATGTTCTTATGTGGAATTTTACCATTGTTGATGATGA 805
DB 620 ATGGAGCATGGGGTTATTTCTCTATGCTTTATTTATGTGGAACCCCTTCCATTTGATGATGA 679
QY 806 TAATGTAATGGCTTTATACAAGAATATGAGAGCAAAATATGATGTTTCCCAAGTGGCT 865
DB 680 CCAATGTGCCACTCTTTTAAAGAGATATGTGATGGGATCTTCTATACCCCTCAATATTT 739
QY 866 CTCTCCAGTAGCATCTGCTTTCTTCAACAAATGTGCAAGGTGGACCCCAAGAAACGGAT 925
DB 740 AAATCCTTCTGTGATTAGCCCTTTTGAACATATATGTCAGAGTGGATCCCATGAAGGGGC 799
QY 926 TTCTATGAAAATCTATTGAACCATCCCTGGATCATGCAAGA---TTACAACTATCTCTGT 982
DB 800 CTCAATCAAGATATCAGGGAACATGAATGGTTTAAACAGGACCTTCCAAAAATATCTCTT 859

Qy 983 TGAGTGGCAAGCAGAAATCCTTTTATTCACCTCGATGATGATGCGTAACAGAACTTTC 1042
Db 860 TCCTGGGATCCATCATATAGTTCACCATGATGATGATGAAGCCTTAAAGAGGTATG 919

Qy 1043 TGTACA 1048
Db 920 TGAATA 925

Search completed: November 21, 2006, 23:04:41
Job time : 561 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications New databases; older published applications make up the Published_Applications Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **rnpbm** (Published_Applications_NA_Main) and **rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **rapbm** (Published_Applications_AA_Main) and **rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: November 21, 2006, 14:04:56 ; Search time 308 Seconds
(without alignments)

1955.147 Million cell updates/sec

Title: US-10-656-598-2

Perfect score: 3447

Sequence: 1 MKDYDELLKYYELHETIGT.....KGDANVYKRLVEDILSSCKV 651

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.2*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3447	100.0	651	1 MELK_HUMAN	Q14680 homo sapien
2	3443	99.9	650	2 Q5T263_HUMAN	Q5T263 homo sapien
3	3443	99.9	651	2 Q53GX0_HUMAN	Q53GX0 homo sapien
4	2878	83.5	643	2 Q3UMB0_MOUSE	Q3UMB0 mus musculus
5	2864	83.1	643	1 MELK_MOUSE	Q61846 mus musculus
6	2863	83.1	643	2 Q3TUF3_MOUSE	Q3TUF3 mus musculus
7	2863	83.1	643	2 Q3TPU1_MOUSE	Q3TPU1 m 12 days e
8	2859	82.9	643	2 Q5U440_MOUSE	Q5U440 mus musculus
9	2852	82.7	643	2 Q3TU15_MOUSE	Q3TU15 mus musculus
10	2348	68.1	457	2 Q4R6B9_MACFA	Q4R6B9 macaca fasc
11	2228	64.6	457	2 Q91821_XENLA	Q91821 xenopus lae
12	2083	60.4	657	2 Q5ZL85_CHICK	Q5ZL85 gallus gall
13	1920	55.7	676	2 Q7Z2N5_BRARE	Q7Z2N5 brachydanio
14	1911	55.4	676	2 Q7ZU72_BRARE	Q7ZU72 brachydanio
15	1528.5	44.3	476	2 Q498M1_XENLA	Q498M1 xenopus lae
16	1307.5	37.9	689	2 Q4RK91_TETNG	Q4RK91 tetraodon n
17	1187.5	34.5	688	2 Q95UF4_ANCCA	Q95UF4 ancylostoma
18	1156	33.5	726	2 Q9UAY1_CAEEL	Q9UAY1 caenorhabdi
19	1128.5	32.7	701	2 Q6U4C7_CAEHR	Q6U4C7 caenorhabdi
20	1071.5	31.1	722	2 Q86FM0_CAEEL	Q86FM0 caenorhabdi
21	804.5	23.3	729	2 Q5U5B2_XENLA	Q5U5B2 xenopus lae
22	792.5	23.0	753	1 MARK3_MOUSE	Q03141 mus musculus
23	791	22.9	744	2 Q9JKE5_MOUSE	Q9JKE5 mus musculus
24	789.5	22.9	783	2 Q5BL77_XENTR	Q5BL77 xenopus tro
25	788.5	22.9	797	1 MARK3_RAT	Q8VH01 rattus norv
26	780.5	22.6	780	2 Q804T1_XENLA	Q804T1 xenopus lae
27	778.5	22.6	725	2 Q804T2_XENLA	Q804T2 xenopus lae
28	775.5	22.5	776	2 Q7ZVL7_XENLA	Q7ZVL7 xenopus lae
29	775	22.5	785	2 Q8QGV3_XENLA	Q8QGV3 xenopus lae
30	767.5	22.3	788	1 MARK2_HUMAN	Q7KX17 homo sapien
31	766.5	22.2	722	2 Q802W0_BRARE	Q802W0 brachydanio

32	764	22.2	776	1 MARK3_HUMAN	P27448 homo sapien
33	759.5	22.0	722	1 MARK2_RAT	Q08679 rattus norv
34	757	22.0	1075	2 Q95U75_DROME	Q95U75 drosophila
35	755.5	21.9	743	2 Q3T9A3_MOUSE	Q3T9A3 mus musculus
36	755.5	21.9	743	2 Q3U3A1_MOUSE	Q3U3A1 mus musculus
37	754.5	21.9	1138	2 Q7KRK3_DROME	Q7KRK3 drosophila
38	753.5	21.9	780	2 Q571J8_MOUSE	Q571J8 mus musculus
39	751	21.8	731	2 Q3T9L3_MOUSE	Q3T9L3 mus musculus
40	751	21.8	905	2 Q7KRK5_DROME	Q7KRK5 drosophila
41	745.5	21.6	795	1 MARK1_HUMAN	Q9P012 homo sapien
42	743.5	21.6	795	1 MARK1_MOUSE	Q8VHJ5 mus musculus
43	742.5	21.5	793	1 MARK1_RAT	Q08678 rattus norv
44	741	21.5	792	2 Q6INT7_XENLA	Q6INT7 xenopus lae
45	738.5	21.4	938	2 Q9V8V8_DROME	Q9V8V8 drosophila

ALIGNMENTS

RESULT 1
ID MELK_HUMAN STANDARD; PRT; 651 AA.
AC Q14680; Q7L3C3;
DT 19-JUL-2004, integrated into UniProtKB/Swiss-Prot.
DT 19-JUL-2004, sequence version 3.
DE Maternal embryonic leucine zipper kinase (EC 2.7.1.37) (hMELK)
DE (Protein kinase PK38) (hPK38).
GN Name=MELK; Synonyms=KIAA0175;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND TISSUE SPECIFICITY.
RC TISSUE=Bone marrow;
RX MEDLINE=96281124; PubMed=8724849; DOI=10.1093/dnares/3.1.17;
RA Nagase T., Seki N., Ishikawa K., Tanaka A., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. V.
RT The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced by
RT analysis of cDNA clones from human cell line KG-1.";
RL DNA Res. 3:117-24 (1996).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins P.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP INTERACTION WITH ZNF622, AND PHOSPHORYLATION OF ZNF622.
RC TISSUE=Keratinocyte;
RX PubMed=11802789; DOI=10.1042/0264-6021:3610597;
RA Seong H.-A., Gil M., Kim K.-T., Kim S.-J., Ha H.;
RT "Phosphorylation of a novel zinc-finger-like protein, ZPR9, by murine

RP NUCLEOTIDE SEQUENCE.
RA Garner P.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AL442063; CAIL1034.1; JOINED; Genomic DNA.
DR EMBL; AL442063; CAIL16995.1; -; Genomic DNA.
DR EMBL; AL354932; CAIL16995.1; JOINED; Genomic DNA.
DR EMBL; AL354932; CAIL1034.1; -; Genomic DNA.
DR Ensembl; ENSG00000165304; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON_TER 650
SQ SEQUENCE 650 AA; 74543 MW; 705CDC6122E5703E CRC64;

Query Match 99.9%; Score 3443; DB 2; Length 650;
Best Local Similarity 100.0%; Pred. NO. 1.2e-223;
Matches 650; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDYDELLKYYELHETIGTGPAKVKLACHILGEMVAIKIMDKNTLGSPLPRIKTEIEA 60
DB 1 MKDYDELLKYYELHETIGTGPAKVKLACHILGEMVAIKIMDKNTLGSPLPRIKTEIEA 60

QY 61 LKVLRHQICQLVHVLTANKIPWLEYCPGBELFYIISQDRLSEETRVVFRQIVSAV 120
DB 61 LKVLRHQICQLVHVLTANKIPWLEYCPGBELFYIISQDRLSEETRVVFRQIVSAV 120

QY 121 AVHSGYAHRLDKPENLLPDEYHKLKIDFGICAKPKGNKDYHLOTCCGSLAYAAPELI 180
DB 121 AVHSGYAHRLDKPENLLPDEYHKLKIDFGICAKPKGNKDYHLOTCCGSLAYAAPELI 180

QY 181 QGKSYLGSEADVMSGILLYVLMCGFLPFDDDNVMALYKKIMRGKYDVPKWLSPSSILL 240
DB 181 QGKSYLGSEADVMSGILLYVLMCGFLPFDDDNVMALYKKIMRGKYDVPKWLSPSSILL 240

QY 241 QQMLQVDPKKRISMKNLNHPWTIMQDYNYPVEWQSKNPPFHLDDCCVTELSVHHRNRQT 300
DB 241 QQMLQVDPKKRISMKNLNHPWTIMQDYNYPVEWQSKNPPFHLDDCCVTELSVHHRNRQT 300

QY 301 MEDLISLMQYDHLTATYLLILLAKARGKPVRLSLSSFCQASATPTDIKSNWLSLEDV 360
DB 301 MEDLISLMQYDHLTATYLLILLAKARGKPVRLSLSSFCQASATPTDIKSNWLSLEDV 360

QY 361 TASDKKNVAGLIDYDWCEDDLSTGAATPRTSQFTKWTESNGVESKSLTPALCRTLPA 420
DB 361 TASDKKNVAGLIDYDWCEDDLSTGAATPRTSQFTKWTESNGVESKSLTPALCRTLPA 420

QY 421 KKNENYTPKSAVKNEEYFMFPPEKTPVKNQKHREILITTPNRYTTPSKARNQCLKETPI 480
DB 421 KKNENYTPKSAVKNEEYFMFPPEKTPVKNQKHREILITTPNRYTTPSKARNQCLKETPI 480

QY 481 KIPVNSTGTDLKMTGVISPERRCRSVELDLNOAHMEETPKRGAKVFGSLERGLDKVITV 540
DB 481 KIPVNSTGTDLKMTGVISPERRCRSVELDLNOAHMEETPKRGAKVFGSLERGLDKVITV 540

Db 481 KIPVNSTGTDLKMTGVISPERRCRSVELDLNOAHMEETPKRGAKVFGSLERGLDKVITV 540
QY 541 LTRSKKSGSARDGPRRLKLYHNVTTTTLVNPQLLNEIMSLIPKQHVDVQKGYTLKCQT 600
DB 541 LTRSKKSGSARDGPRRLKLYHNVTTTTLVNPQLLNEIMSLIPKQHVDVQKGYTLKCQT 600

QY 601 QSDFGKVTWQFLEVCQLOKPDVVGIRRRORLKGDAWVYKRLVEDILSSCK 650
DB 601 QSDFGKVTWQFLEVCQLOKPDVVGIRRRORLKGDAWVYKRLVEDILSSCK 650

RESULT 3
Q53GX0_HUMAN PRELIMINARY; PRT; 651 AA.
AC Q53GX0;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-PEB-2006, entry version 6.
DE Maternal embryonic leucine zipper kinase variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA MEDLINB-94171032; PubMed=8125298; DOI=10.1016/0378-1119(94)90802-8;
RX Maruyama K., Sugano S.;
RT "Oligo-capping: a simple method to replace the cap structure of
RT eucaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE-9803896; PubMed=9373149; DOI=10.1016/S0378-1119(97)00411-3;
RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-
RL end-enriched cDNA library.";
RL Gene 200:149-156(1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
RA Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AK222811; BAD96531.1; -; mRNA.
DR Ensembl; ENSG00000165304; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON_TER 1

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yang Y., Yang L., Yang L.,
RA Yuan Z., Zavan L.M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume M., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Saeki K., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldi M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Maehima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690 (2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630 (2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Itoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplexed capillary sequencer";
RL Genome Res. 10:1757-1771 (2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Itoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplexed capillary sequencer";
RL Genome Res. 10:1757-1771 (2000).
RN [9]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Itoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplexed capillary sequencer";
RL Genome Res. 10:1757-1771 (2000).
RN [10]
RP NUCLEOTIDE SEQUENCE.
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CC EMBL; AK145021; BAE26188.1; -, mRNA.
DR MGI; MGI:106924; Melk.
DR GO; GO:0005773; C:cytoplasm; IDA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; RCA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; RCA.
DR InterPro; IPR001772; Kinase.C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; Kinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN_1.
KW ATP-binding; kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 643 AA; 72727 MW; 0451D6BE81D4AE5A CRC64;
Query Match 83.5%; Score 2878; DB 2; Length 643;
Best Local Similarity 83.7%; Pred. No. 1.6e-185;
Matches 545; Conservative 44; Mismatches 54; Indels 8; Gaps 2;
QY 1 MKDYDELLKYELHETIGTGGFAKVKLACHILTGMVAIKIMDKNTGLSGDLPRIKTEIFA 60
DB 1 MKDYDELLKYELHETIGTGGFAKVKLACHILTGMVAIKIMDKNTGLSGDLPRIKTEIFA 60
QY 61 LKSLRQHIHQYHVLVETANKIFMVLVPCGELFDYIISQDLSEETRVVFRQIVSAV 120
DB 61 LKSLRQHIHQYHVLVETANKIFMVLVPCGELFDYIISQDLSEETRVVFRQIVSAV 120
QY 121 AVVHSGYAHRLDKPENLLFDYHKLKLDIFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180
DB 121 AVVHSGYAHRLDKPENLLFDYHKLKLDIFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180
QY 181 QGKSYLGSEADVWSMGILLIYLMCGFLPDDDDNNVVALYKKIMRGKYDVPKWLSPSSILL 240
DB 181 QGKSYLGSEADVWSMGILLIYLMCGFLPDDDDNNVVALYKKIMRGKYDVPKWLSPSSILL 240
QY 241 QOMLVDPKRIKSMKLNHNMIMODYVPMQSKNPFILHDDCVTELSSHHRNROT 300
DB 241 QOMLVDPKRIKSMKLNHNMIMODYVPMQSKNPFILHDDCVTELSSHHRNROT 300
QY 301 MEDLISLWOYDHLTATYLLALLAKAKGKPVRLSLSFSCQASATPFTDIKSNWLSLDV 360
DB 301 MEDLISLWOYDHLTATYLLALLAKAKGKPVRLSLSFSCQASATPFTDIKSNWLSLDV 360
QY 361 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSFTKYWTESNGVESKSLTPALCPTPANKL 420
DB 361 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSFTKYWTESNGVESKSLTPALCPTPANKL 420
QY 421 KXKENVYTPKSAVKEEYPMPEPKTPKTNQKHREILLTPNRYTTPSKARNOCLKETPI 480
DB 421 KXKENVYTPKSAVKEEYPMPEPKTPKTNQKHREILLTPNRYTTPSKARNOCLKETPI 480
QY 481 KIPVNSTGTDLKMTGVISPERCSRVELDLNOAHMEETPKRGAKVFGSLERGLDKVITV 540
DB 481 KIPVNSTGTDLKMTGVISPERCSRVELDLNOAHMEETPKRGAKVFGSLERGLDKVITV 540
QY 541 LTRSKRGSGARDPRRLKLVNVTTLVNPOLLNEIMSLPKGHVDPVQGYTLKCT 600
DB 541 LTRSKRGSGARDPRRLKLVNVTTLVNPOLLNEIMSLPKGHVDPVQGYTLKCT 600
QY 601 QSDFGKVTQFLEVCOLQPDVVGIRORLKGDAWVKRLVEDILSSCKV 651
DB 601 QSDFGKVTQFLEVCOLQPDVVGIRORLKGDAWVKRLVEDILSSCKV 651
QY 651 QSDFGKVTQFLEVCOLQPDVVGIRORLKGDAWVKRLVEDILSSCKV 651
DB 651 QSDFGKVTQFLEVCOLQPDVVGIRORLKGDAWVKRLVEDILSSCKV 651
RESULT 5
ID MELK_MOUSE STANDARD; PRT; 643 AA.

AC O61846; Q61804; Q6ZQH6;
DT 19-JUL-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-MAR-2006, entry version 42.
DE Maternal embryonic leucine zipper kinase (EC 2.7.1.37) (Protein kinase
DE PK38) (mpk38).
GN Name:Melk; Synonym:Klaa0175, PK38;
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
RC TISSUE=teratocyst;
RX MEDLINE=97449306; PubMed=9305775; DOI=10.1016/S0378-1119(97)00181-9;
RA Gil M., Yang Y., Lee Y., Choi I., Ha H.;
RT "Cloning and expression of a cDNA encoding a novel protein
RT serine/threonine kinase predominantly expressed in hematopoietic
RT cells.";
RL Gene 195:295-301(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA], TISSUE SPECIFICITY, AND DEVELOPMENTAL
RP STAGE.
RC STRAIN=C57BL/6 X DBA/2;
RX PubMed=9136115;
RX DOI=10.1002/(SICI)1098-2795(199706)47:2<148::AID-MRP4>3.0.CO;2-M;
RA Oyama R., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Carninci P., Kasukawa T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Attaliya R.N., Bailey T.L.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailetti T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhury V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dall'Amico B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustigich S., Harbers M., Hayashizaki Y., Hensch T.K., Hirokawa N.,
RA Hilt D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jaki M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.P., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakaochi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Sheng Y.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tsgami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";

RL Science 309:1559-1563(2005).
[4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Embryonic tail;
RX MEDLINE=22977043; PubMed=14621295; DOI=10.1093/dnares/10.4.167;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT III. The complete nucleotide sequences of 500 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:167-180(2003).
CC -!- FUNCTION: Phosphorylates ZNF622 and may contribute to its
CC redirection to the nucleus. May be involved in the inhibition of
CC spliceosome assembly during mitosis (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Interacts with ZNF622 and PPIR8 (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasm (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in testis, ovary, thymus, spleen and
CC T-cell.
CC -!- DEVELOPMENTAL STAGE: Expressed in the 2-cell-stage embryo,
CC followed by a strong expression at 8-cell-stage.
CC -!- PTM: Autophosphorylated (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. SNF1
CC subfamily.
CC -!- SIMILARITY: Contains 1 KAI (kinase-associated) domain.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; L76158; AAB72030.1; -; mRNA.
DR EMBL; X95351; CAA64641.1; -; mRNA.
DR EMBL; AK011932; BAB27923.1; -; mRNA.
DR EMBL; AK129076; BAC97886.1; -; mRNA.
DR HSSP; Q63450; 1A06.
DR MGI; MGI:106924; Melk.
DR GO; GO:0005737; Cytoplasm; IDA.
DR GO; GO:004672; F:protein kinase activity; IDA.
DR InterPro; IPR001772; Kinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_kin_AS.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-Binding; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT CHAIN 1 643 Maternal embryonic leucine zipper kinase.
FT /FTID=PRO_0000086324.
FT DOMAIN 11 263 Protein kinase.
FT DOMAIN 594 643 KAI.
FT NP_BIND 17 25 ATP (By similarity).
FT ACT_SITE 132 132 Proton acceptor (By similarity).
FT BINDING 40 40 ATP (By similarity).
FT CONFLICT 335 335 P -> L (in Ref. 3).
SQ SEQUENCE 643 AA; 72713 MW; 411792A8A19FE213 CRC64;
Query Match 83.1%; Score 2864; DB 1; Length 643;
Best Local Similarity 83.3%; Pred. No. 1.4e-184;
Matches 542; Conservative 45; Mismatches 56; Indels 8; Gaps 2;
QY 1 MKDYDELLKYELHETIGTGGFAKVKLACHILITGEMVAIKMDKNTLGSGLPRIKTEIEA 60
Db 1 MKDYDELLKYELHETIGTGGFAKVKLACHILITGEMVAIKMDKNTLGSGLPRIKTEIEA 60
QY 61 LKNLRHGHICQLHYVLETKNKIFMWLEYCPGGELEFDYIISQDLSEETRVVPRQIVSAV 120
Db 61 LKSLRHGHICQLHYVLETKNKIFMWLEYCPGGELEFDYIISQDLSEETRVVPRQIVSAV 120

QY 121 AYVHSQGYAHRDLKPENLLFDEYHKLIDFGLCAKPKGNKVHLOTCGSSLAYAAPALI 180
 DB 121 AYVHSQGYAHRDLKPENLLFDEYHKLIDFGLCAKPKGNKVHLOTCGSSLAYAAPALI 180
 QY 181 QGKSYLGSEADVMSGILLVYVLCGFLPFDDNNMAYLYKKIMRGKYDVPKWLSPSSLLLL 240
 DB 181 QGKSYLGSEADVMSGILLVYVLCGFLPFDDNNMAYLYKKIMRGKYDVPKWLSPSSLLLL 240
 QY 241 QOMLQVDPKCRISMRNLNHPWIMQDYNYPVQSKNPFTHLDDDCVTELSVHRRNRQT 300
 DB 241 QOMLQVDPKCRISMRNLNHPWIMQDYNYPVQSKNPFTHLDDDCVTELSVHRRNRQT 300
 QY 301 MEDLISLWQYDHTATYVLLLLAKARGKPVRLBSFSCQQAATPFTDCKSNWSLEVDV 360
 DB 301 MEDLISLWQYDHTATYVLLLLAKARGKPVRLBSFSCQQAATPFTDCKSNWSLEVDV 360
 QY 361 TASDKNVVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTEGVSGLTLPALCRTCRTANKL 420
 DB 361 TASDKNVVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTEGVSGLTLPALCRTCRTANKL 420
 QY 421 KXKENVYTPKSAVKNBEYFMPPFKTPVKNQKHREILITTPNRYTTPSKARNQCLKETPI 480
 DB 421 KXKENVYTPKSAVKNBEYFMPPFKTPVKNQKHREILITTPNRYTTPSKARNQCLKETPI 480
 QY 481 KIPVNSTGTDKMTGVISPPRRCSRVELDLNOAHMBETPKRGAQVFGSLERGLDKVITV 540
 DB 481 KIPVNSTGTDKMTGVISPPRRCSRVELDLNOAHMBETPKRGAQVFGSLERGLDKVITV 540
 QY 473 RTPGNSAGADTLTGTGVSPPRRCSRVDVLNOAHMEDTPKKGNTVFGSLERGLDKVITA 532
 DB 473 RTPGNSAGADTLTGTGVSPPRRCSRVDVLNOAHMEDTPKKGNTVFGSLERGLDKVITA 532
 QY 541 LTRSKRKGSGARDGPRKLKHYNVYVTRLVNPDOLLNEMSLPKKHVDVFKGYTTLKCO 600
 DB 541 LTRSKRKGSGARDGPRKLKHYNVYVTRLVNPDOLLNEMSLPKKHVDVFKGYTTLKCO 600
 QY 601 QSDFGKVTWQFLEVCQKPDVVGIRRORLKGDWVYKRLVEDILSSCKV 651
 DB 601 QSDFGKVTWQFLEVCQKPDVVGIRRORLKGDWVYKRLVEDILSSCKV 651
 QY 593 QSDFGKVTWQFLEVCQKPDVVGIRRORLKGDWVYKRLVEDILSSCKV 643
 DB 593 QSDFGKVTWQFLEVCQKPDVVGIRRORLKGDWVYKRLVEDILSSCKV 643

RESULT 6
 ID Q3TJF3 MOUSE PRELIMINARY; PRT; 643 AA.
 AC Q3TJF3
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 7.
 DE 12 days pregnant adult female placenta cDNA, RIKEN full-length
 DE enriched library, clone:1530014L15 product:maternal embryonic leucine
 DE zipper kinase, full insert sequence.
 GN Name=Mek;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 [2]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RX PubMed=16141072; DOI=10.1126/science.11112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Chiu M.L., Dalla E., Dairymple B.P., de Bono B., Della Gatta G.,

di Bernardo D., Down T., Engstrom P., Pagiolini M., Faulkner G.,
 Fletcher C.P., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
 Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
 Rostrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 Sperling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K.,
 Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 Grimmond S.M., Tesdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Nanomiya N.,
 Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 Hayashizaki Y.
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RX PubMed=16141073; DOI=10.1126/science.11112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kongsaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numa K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Tesdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayashizaki Y.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Iehli Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [5]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaïdo I., Pesole G., Quackenbush J.,
RA Schraml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtauki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: AK167457; BAE39542.1; -; mRNA.
CC MGI: MGI:108924; Melk.
CC GO: GO:0005737; C:cytoplasm; IDA.
CC GO: GO:0004713; P:protein-tyrosine kinase activity; RCA.
CC InterPro: IPR001772; Kinase C.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR008271; Ser_thr_pkin_AS.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC InterPro: IPR001245; Tyr_pkinase.
CC Pfam: PF02149; KAI; 1.
CC Pfam: PF00069; Pkinase; 1.
CC ProDom: PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; transferase;
SQ SEQUENCE 643 AA; 72757 MW; ADA9240C6C5GFA4 CRC64;
Query Match 83.1%; Score 2863; DB 2; Length 643;
Best Local Similarity 83.3%; Pred. No. 1.6e-184;
Matches 542; Conservative 45; Mismatches 56; Indels 8; Gaps 2;
QY 1 MKDYDELLKYYELHETITGTGGFAKVLACHILITGEMVAIKIMDKNTLGSDDLPRITKEIFA 60
DB 1 MKDYDELLKYYELHETITGTGGFAKVLACHILITGEMVAIKIMDKNTLGSDDLPRVTEIDA 60
QY 61 LKVLRHQHICQLYHVLETKNKFIMVLEPCPGELFDYIISQDLSEETRVVPRQIVSAV 120
DB 61 LKSLRHQHICQLYHVLETKNKFIMVLEPCPGELFDYIISQDLSEETRVVPRQLLSAV 120
QY 121 AVVHSGQVAHRLDKPENLLFDYVHKLKIDFGLCAKPGKNDYHQLTCCGSLAYAAPELI 180
DB 121 AVVHSGQVAHRLDKPENLLFDENHKLKIDFGLCAKPGKNDYHQLTCCGSLAYAAPELI 180
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DB 241 QOMLQVDPKRI:SMRNLNHPWMDYSCPVWQSKNPTLTHLDEDCVTSLVHHRRSROT 300
QY 301 MEDLISLMQYDHLTATYLLLLAKKARGKPVRLURLSSFCQASATPFTDIKSNNSLEDV 360
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DB 357 STSDDDNCVAGLIDYELCEDKL---LAPKTPQVTKHLAESNHAASKSPAGVRRVAVANKL 412
QY 421 KKNENYTPKSAVQVEEYPMPEPKTPYQKQKHEILLTPNRYTTPSKARNOCLKETPI 480
DB 413 MDKENVCTPKSVQVEEQVFSEPKIPVSKNKYKKEIPASPTFRFPFPKARQAQCLKEAPV 472
QY 481 KLPVNSTGTDKLMGTGVISPERCSRVELDLNOAHMEETPKRGAKVFGSLERGLDKVITV 540
DB 473 RFPGNSAGADTLTTGVISPERCSRWDVDLNOAHMEDTPKKGTVNFGSLERGLDKVITA 532
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DB 533 LTRNKKKGSGARDGPRKRLKLYHNVTTTLVNPDLNLEIMAILPKKNVDFVQKGYTLKCOQT 592
QY 601 QSDFGKVTWQFLEVCQLOKQPDVVGIRRRORLKGDAWYKRLVEDILSSCKV 651
DB 593 QSDFGKVTWQFLEVCQLOKQRPDVVGIRRRORLKGDAWYKRLVEDILSSCKM 643
RESULT 7
Q3TPUL_MOUSE PRELIMINARY; PRT; 643 AA.
ID Q3TPUL_MOUSE AC Q3TPUL;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE 12 days embryo spinal cord cDNA, RIKEN full-length enriched library,
DE clone: C530047P3 product: maternal embryonic leucine zipper kinase,
DE full insert sequence (4 cells embryo 4 cells cDNA, RIKEN full-length
DE enriched library, clone: I0C0001106 product: maternal embryonic leucine
DE zipper kinase, full insert sequence).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama T., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Zvolansek A., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Adkins J.E., Ambesi-Impombato A., Arweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., Di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G., Petrovsky N., Piazza S., Reed J.C., Reid J.P., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Sempile C.A., Seno S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K., Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki K., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashina T., Koike M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the PANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [4]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., RA Blakes L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., RA Gaasterland T., Gariboldi M., Glissi C., Godzik A., Gough J., RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RN [9]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs license
CC -----
DR EMBL; AK164138; BAE37644.1; -; mRNA.
DR EMBL; AK145316; BAE26362.1; -; mRNA.
DR GO; GO:0005737; Cytoplasm; IDA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; RCA.
DR InterPro; IPR001772; Kinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 643 AA; 72729 MW; 5637D2A4E8CFA216 CRC64;

Query Match 83.1%; Score 2863; DB 2; Length 643;
Best Local Similarity 83.3%; Pred. No. 1.6e-184;
Matches 542; Conservative 45; Mismatches 56; Indels 8; Gaps 2;

QY 1 MKDYDELLKYELHETIGTGGFAVKVLACHILTGENVAIKIMDKNTLGSDELPRKTEIBA 60
DB 1 MKDYDELLKYELYETIGTGGFAVKVLACHVLTGENVAIKIMDKNALGSDLPVKTEIDA 60

QY 61 LKNLRHQHCQLYHVLETANKIPWLEYCPGGBLPDYIISQDLSEETRVVPRQIVSAV 120
DB 61 LKSLRHQHCQLYHVLETANKIPWLEYCPGGBLPDYIISQDLSEETRVVPRQIVSAV 120

QY 121 AVVHSGYAHRLDKPENLLFDEYHKLIDFGLCAPKGNKDYHLQTCGSLAYAAPELI 180
DB 121 AVVHSGYAHRLDKPENLLFDEYHKLIDFGLCAPKGNKDYHLQTCGSLAYAAPELI 180

QY 181 QGKSYLGSEADVMSGILLYVLMCGFLPFDDDDNMALYKIMRGKYDVPKWLSPSSILL 240
DB 181 QGKSYLGSEADVMSGILLYVLMCGFLPFDDDDNMALYKIMRGKYDVPKWLSPSSILL 240

QY 241 QQMLQVDPKRTSMKNLLNHPWIMQDYNVPVEWQSKNPFIHLDDDCVTELSVHHNRQT 300
DB 241 QQMLQVDPKRTSMRNLNHPWIMQDYSQVQSKTPTLTHLDDCVTELSVHHRSRQT 300

QY 301 MEDLISLWQYDHLTATYLLALLAKARGKPVRLRLSFCGQASATPTFTDKSNWLSLEV 360
DB 301 MEDLISLWQYDHLTATYLLALLAKARGKPARLQLLSFCGQASTPT-----KSNLSLED 356

QY 361 TASDKNRYAGLIDYDCEDDLSTGAATPRTSQFTKYWTEGNSGVESKSLTPALCRTPANKL 420
DB 361 TASDKNRYAGLIDYDCEDDLSTGAATPRTSQFTKYWTEGNSGVESKSLTPALCRTPANKL 420

QY 357 STSDNDDCVAGLIDYELCEDK-----LAPKTPQVTKHLAESNHAASKSPAGVGERAVANKL 412
DB 357 STSDNDDCVAGLIDYELCEDK-----LAPKTPQVTKHLAESNHAASKSPAGVGERAVANKL 412

QY 421 KKNENYTPKSAVKNREYFMFPKPTPVNKNQHKRILITPNRYTTPSKARNOCLETPI 480
DB 421 KKNENYTPKSAVKNREYFMFPKPTPVNKNQHKRILITPNRYTTPSKARNOCLETPI 480

QY 413 MDKENYCTPKSSVKNEEQVFSEPKIPVSKNQYKREIPASPTFRPTPAKARAQCLREAPV 472
DB 413 MDKENYCTPKSSVKNEEQVFSEPKIPVSKNQYKREIPASPTFRPTPAKARAQCLREAPV 472

QY 481 KIPVNSTGTDKLMTGVISPERRCSRVELDLNOAHMEETPKRKGAQVFGSLERGLDKVITV 540
DB 473 RTPGNSAGADTLTTGTVISPERRCSRVDVLDLNOAHMEDTPKKGTNVFGSLERGLDKVLT 532

QY 541 LTRSRKRGSGARDGPRRLKLYHNVTTTTLVNPOLLNEIMSLPKKHVDVFGVQGYTLKCO 600
DB 533 LTRNKKGSARDGPRRLKLYHNVTTTTLVNPOLLSEIMAILPKKNVDVFGVQGYTLKCO 592

QY 601 QSDFGKVTMQFLEVCQLQKDPDVGIRRLQKGDGAWYKRLVEDILSSCKV 651
DB 593 QSDFGKVTMQFLEVCQLQKDPDVGIRRLQKGDGAWYKRLVEDILSSCKM 643

RESULT 8
OSU440_MOUSE PRELIMINARY; PRT; 643 AA.
AC OSU440;
DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 1.
DE 07-FEB-2006, entry version 16.
DE Maternal embryonic leucine zipper kinase.
GN Name=Melk;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo; STRAIN=C57BL/6J;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RA Director MGC Project;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs license
CC -----
DR EMBL; BC085276; AAH85276.1; -; mRNA.
DR Ensembl; ENSMUSG0000035683; Mus musculus.
DR MGI; MGI:106924; Melk.
DR GO; GO:0005737; Cytoplasm; IDA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; RCA.
DR InterPro; IPR001772; Kinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF02149; KAI; 1.

DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S TK; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN 1.
 KW ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 643 AA; 72757 MW; 058893D779BDFE17 CRC64;

Query Match 82.9%; Score 2859; DB 2; Length 643;
 Best Local Similarity 83.1%; Pred. No. 3.1e-184;
 Matches 541; Conservative 46; Mismatches 56; Indels 8; Gaps 2;

QY 1 MKDYDELLKYYELHETIGTGGFAKVLACHILGEMVAIKIMDKNTIGSLDPRKIEIEA 60
 DB 1 MKDYDELLKYYELHETIGTGGFAKVLACHILGEMVAIKIMDKNKGSLDPRKVEIDA 60

QY 61 LKMLRHQHCQLHYVLETKANKIFWVLEPCGGLFDYIIISQDRLSEETRVFVRQIVSAV 120
 DB 61 LKSLRHQHCQLHYVLETKANKIFWVLEPCGGLFDYIIISQDRLSEETRVFVRQILSAV 120

QY 121 AYVHSGQYAHRDLPENLLPDEYHKLIDFGICAKPKGNKDVHLOTCCGSLAYAAPELI 180
 DB 121 AYVHSGQYAHRDLPENLLPDEYHKLIDFGICAKPKGNKDVHLOTCCGSLAYAAPELI 180

QY 181 QGKSYLGSEADVMSGILLVLMCGFLPFDNDNMALYKKIMRGKYDVPKWLSPSSILL 240
 DB 181 QGKSYLGSEADVMSGILLVLMCGFLPFDNDNMALYKKIMRGKYDVPKWLSPSSILL 240

QY 241 QQMLQVDPKPKRISMKNLLNHPWIMQDYNYPVWOSKNPFIHLDDDCVTELNVHHRNQT 300
 DB 241 QQMLQVDPKPKRISMKNLLNHPWIMQDYNYPVWOSKNPFIHLDDDCVTELNVHHRNQT 300

QY 301 MEDLISIMQYDHLTATVLLLLAKKAKPKVRLSLSPSCQASATPFTDIKSNWLSLEOV 360
 DB 301 MEDLISIMQYDHLTATVLLLLAKKAKPKVRLSLSPSCQASATPFTDIKSNWLSLEOV 360

QY 361 TASDKNYPVAGLIDYDCEDDLSTGAATPRTSQTQKYWTESNGVESKSLTPALCRTPANKL 420
 DB 361 TASDKNYPVAGLIDYDCEDDLSTGAATPRTSQTQKYWTESNGVESKSLTPALCRTPANKL 420

QY 421 KXENVYTPKSAVNEBYFPPEKTPVKNQKHREILTPNRYTPSKARNOKLKETPI 480
 DB 421 KXENVYTPKSAVNEBYFPPEKTPVKNQKHREILTPNRYTPSKARNOKLKETPI 480

QY 481 KIPVNSTGTDKMTGTVISPERCRSVELDINOAHMETPKKCAKVGSLERGLDKVITV 540
 DB 481 KIPVNSTGTDKMTGTVISPERCRSVELDINOAHMETPKKCAKVGSLERGLDKVITV 540

QY 541 LTRSKRKGSGARDGPRRLKHYNTVTLVNPDLLEIMSLPKKHVDVFKQGYTLKCOQ 600
 DB 541 LTRSKRKGSGARDGPRRLKHYNTVTLVNPDLLEIMSLPKKHVDVFKQGYTLKCOQ 600

QY 601 QSDFGKVTWQFELEVQOLQKPDVVGIRORQLKGDWVYKRLVEDILSSCKV 651
 DB 601 QSDFGKVTWQFELEVQOLQKPDVVGIRORQLKGDWVYKRLVEDILSSCKV 651

QY 593 QSDFGKVTWQFELEVQOLQKPDVVGIRORQLKGDWVYKRLVEDILSSCKM 643

RESULT 9

Q3TU15 MOUSE

ID Q3TU15_MOUSE PRELIMINARY; PRT; 643 AA.

AC Q3TU15;

DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.

DT 11-OCT-2005, sequence version 1.

DT 07-FEB-2006, entry version 7.

DE 14 days embryo liver cDNA, RIKEN full-length enriched library,

DE clone:4432406P16 product:maternal embryonic leucine zipper kinase,

DE full insert sequence.

DE Name=Welk;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 [2]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Liver;
 RC PubMed=16141073; DOI=10.1126/science.1112014;
 RX Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilm M., Djafarzadeh S., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.P., Fukushima T., Furum M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda M., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlandi V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Tesard R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Lida J., Inamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawahina T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 [3]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Liver;
 RC PubMed=16141073; DOI=10.1126/science.1112009;
 RX RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 [4]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Liver;
 RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RX Okazaki Y., Furum M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Otsu N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawai J., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Nagatsuma A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wu L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirokane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=liver;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Koichiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli R., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombardi P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohseki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690 (2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=liver;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630 (2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=liver;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771 (2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=liver;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imanura K., Inotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura N., Ninomiya N.,

RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC - SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonCommercial License
CC
DR EMBL: AK161029; BAE36156.1; -; mRNA.
DR MGI: MGI:106924; Melk.
DR GO: GO:0005737; Cytoplasm; IDA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; RCA.
DR InterPro: IPR001772; Kinase C.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR008271; Ser_Thr_kinase.
DR InterPro: IPR002290; Ser_Thr_kinase.
DR Pfam: PF02149; KAI; 1.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot kinase; 1.
DR SMART: SM00220; S_TKc_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 643 AA; 72787 MW; 1092C14709A64966 CRC64;

Query Match 82.7%; Score 2852; DB 2; Length 643;
Best Local Similarity 82.9%; Pred. No. 9.1e-184;
Matches 540; Conservative 46; Mismatches 57; Indels 8; Gaps 2;

QY 1 MKDYDELLKYYELHETIGTGGFAKVKLACHITGEMVAIKIMDKNTLGLDPRKTEIRA 60
DB 1 MKDYDELLKYYELHETIGTGGFAKVKLACHITGEMVAIKIMDKNTLGLDPRKTEIRA 60
QY 61 LKNLRHQHICOLYHVLETKANKIFMWLEVCYCGELFDYIISQDRLSEETRVVFRQIVSAV 120
DB 61 LKSLRHQHICOLYHVLETKANKIFMWLEVCYCGELFDYIISQDRLSEETRVVFRQIVSAV 120
QY 121 AYVHSGVYAHRLKPEENLLFDYHKLKLDIFGLCAKPKGNKYHLQTCGSLAYAAPELI 180
DB 121 AYVHSGVYAHRLKPEENLLFDYHKLKLDIFGLCAKPKGNKYHLQTCGSLAYAAPELI 180
QY 181 QGKSYLGSEADYVSMGILLYVLMCGFLPDDNNVALYKKIMRGKYDVPKWLSPSSILL 240
DB 181 QGKSYLGSEADYVSMGILLYVLMCGFLPDDNNVALYKKIMRGKYDVPKWLSPSSILL 240
QY 241 QQMLQVDPKKRISMKNLNHPIMQDYNYPVEWQSKNPFILHDDDCVTELSVHRRNRQT 300
DB 241 QQMLQVDPKKRISMRNLNHPVMDYSCFVEMQSKTPTLHLDDECVTELSVHRRNRQT 300
QY 301 MEDLISLMQYDHLTATYLLLLAKKARGKPVRLURLSFCGQASATPFTDIKSNWMSLEDV 360
DB 301 MEDLISLMQYDHLTATYLLLLAKKARGKPVRLURLSFCGQASATPFTDIKSNWMSLEDV 360
QY 361 TASDKNYVAGLDYDWCEDDLTGATPRTSQFTKYWTSNGVSKSLTPALCRTPANKL 420
DB 361 TASDKNYVAGLDYDWCEDDLTGATPRTSQFTKYWTSNGVSKSLTPALCRTPANKL 420
QY 357 STSDNDCVAGLDYELCEDKL----LAPKTPQVTKHLSNHAASKSPAGVRAVANKL 412
DB 357 STSDNDCVAGLDYELCEDKL----LAPKTPQVTKHLSNHAASKSPAGVRAVANKL 412
QY 421 KKNENYVTPKSAVQNEEYFMFPEPKTPVKNKHQKREILTTPNRYTTPSKARNQCKETPI 480
DB 421 KKNENYVTPKSAVQNEEYFMFPEPKTPVKNKHQKREILTTPNRYTTPSKARNQCKETPI 480
QY 413 MDKENVCTPKSSVQNEEQVFSEPKIPVSKNQYKREIPASPTFFTPAKARAQCLREAPV 472
DB 413 MDKENVCTPKSSVQNEEQVFSEPKIPVSKNQYKREIPASPTFFTPAKARAQCLREAPV 472
QY 481 KIPVNSTGTDKLMTGTVISPERCSRVELDLNOAHMEETPKRGAKVFGSLRGGLDKVITV 540
DB 481 KIPVNSTGTDKLMTGTVISPERCSRVELDLNOAHMEETPKRGAKVFGSLRGGLDKVITV 540
QY 473 RTPGNSAGADTLTTGTVISPERCSRSDVDLNOAHMEDTPKKGKGTNVFGSLRGGLDKVITV 532
DB 473 RTPGNSAGADTLTTGTVISPERCSRSDVDLNOAHMEDTPKKGKGTNVFGSLRGGLDKVITV 532
QY 541 LTRSKKSGSARDGPRELKLHYNTVTTTRLVNPQDLNEIMSILPKKHVDVFKQGYTLKCO 600
DB 541 LTRSKKSGSARDGPRELKLHYNTVTTTRLVNPQDLNEIMSILPKKHVDVFKQGYTLKCO 600
QY 533 LTRNKKKSGSARDGPRKRLHYNTVTTTRLVNPQDLNEIMSILPKKHVDVFKQGYTLKCO 592
DB 533 LTRNKKKSGSARDGPRKRLHYNTVTTTRLVNPQDLNEIMSILPKKHVDVFKQGYTLKCO 592

QY 601 QSDPGKVTWQFEVLEVCOLQKPDVVGIRRRQLKGDWVYKLVEDILSSCKV 651
 DB 593 QSDPGKVTWQFEVLEVCOLQKPDVVGIRRRQLKGDWVYKLVEDILSSCKM 643

RESULT 10
 Q4R6B9 MACFA
 ID Q4R6B9_MACFA PRELIMINARY; PRT; 457 AA.
 AC Q4R6B9;
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Testis cDNA, clone: Q4R6B9-18422, similar to human maternal embryonic
 DE leucine zipper kinase (MLK).
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15944441; DOI=10.1093/molbev/msi187;
 RA Oeada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
 RA Sugano S., Gojobori T., Shen C.-K.J., Wu C.-I., Hashimoto K.,
 RT "Substitution Rate and Structural Divergence of 5'UTR Evolution:
 RT Comparative Analysis Between Human and Cynomolgus Monkey CDNA's";
 RL Mol. Biol. Evol. 22:1976-1982(2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG International consortium for macaque cDNA sequencing and analysis;
 RT "DNA sequences of macaque genes expressed in brain or testis and its
 RT evolutionary implications";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DB EMBL; AB169266; BAE01356.1; -; mRNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:000166; F:nucleotide binding; IEA.
 DR GO; GO:004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:000468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR001772; Kinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR Pfam; PF02149; KAI; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Kinase; Nucleotide-binding; Transferase.
 SQ SEQUENCE 457 AA; 52621 MW; CA48A54A164022F0 CRC64;

Query Match 68.1%; Score 2348; DB 2; Length 457;
 Best Local Similarity 97.2%; Pred. No. 6.1e-150;
 Matches 444; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 195 MGLLYVLMCGFLPFDDNNMALYKIMRGKVDVVKWLSFSSILLQQLQVDPKKRISM 254
 DB 1 MGLLYVLMCGFLPFDDNNMALYKIMRGKVDVVKWLSFSSILLQQLQVDPKKRISM 60
 QY 255 KNLLNHPWIMQDYNYPVEWQSKNPFHLLDDCVTELSVHRRNRQTMEDLISLWQYDHLT 314
 DB 61 KNLLNHPWIMQDYNYPVEWQSKNPFHLLDDCVTELSVHRRNRQTMEDLISLWQYDHLT 120
 QY 315 ATYLLLLAKKRGKPVRLRLSFCQASATPFTDIKSNWSLEDVTASDKNVAGLIDY 374
 DB 121 ATYLLLLAKKRGKPVRLRLSFCQASATPFTDIKSNWSLEDVTASDKNVAGLIDY 180
 QY 375 DWCEDDLSTGAATPRTSQFTKYTESNGVESKSLTPALCRTPANKLNKENYVTPKSAVK 434
 DB 181 DWYEDNLSTGAATPQKSTQFTKYTESNGVESKSLTPALCRTPANKLNKENYVTPKSAVK 240
 QY 435 NEEYFMFPFKPTPVNKHQKREILTPNRYATPFSKARNOCCLKETPIKMPVNSTGTDKLMT 494

DB 241 NEEYFMFPFKPTPVNKHQKREILTPNRYATPFSKARNOCCLKETPIKMPVNSTGTDKLMT 300
 QY 495 GVISPERRCRSVELDLNQAHMEETPKRGAKVFGSLERGLDKVITVLTSTRKRGSGARDGP 554
 DB 301 GVISPERRCRSVELDLNQAHMEETPKRGAKVFGSLERGLDKVITVLTSTRKRGSGARDGP 360
 QY 555 RLKLHYNVTTRLVNPDQLINEIMSLPKKVDVFKQGYTLKCTQSDFGKVTMQFELE 614
 DB 361 RLKLHYNVTTRLVNPDQLINEIMSLPKKVDVFKQGYTLKCTQSDFGKVTMQFELE 420
 QY 615 VCQLOKPDVVGIRRRQLKGDWVYKLVEDILSSCKV 651
 DB 421 VCQLOKPDVVGIRRRQLKGDWVYKLVEDILSSCKV 457

RESULT 11
 Q91821 XENLA
 ID Q91821_XENLA PRELIMINARY; PRT; 651 AA.
 AC Q91821;
 DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2001, sequence version 2.
 DT 07-FEB-2006, entry version 39.
 DE P69Bg3 (Hypothetical protein).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Unfertilized eggs;
 RA Roghi C., Le Guellec R., Paris J., Couturier A., Philippe M.;
 RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Unfertilized eggs;
 RA Tassan J.P.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Oocytes;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Oocytes;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lomellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.

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RC TISSUE=Oocytes;
RA Klein S., Gerhard D.S.;
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
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CC -----
DR EMBL; Z17205; CAA78913.2; -; mRNA.
DR EMBL; BC106635; AAI06636.1; -; mRNA.
DR FIR; S52244; S52244.
DR HSSP; P49137; 1NY3.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 651 AA; 74307 MW; A21B397D0F1A9C9A CRC64;

Query Match 64.6%; Score 2228; DB 2; Length 651;
Best Local Similarity 65.2%; Pred. No. 1.2e-141;
Matches 427; Conservative 90; Mismatches 124; Indels 14; Gaps 8;

QY 3 DYDELLKYYELHETIGTGFGPAKVKLACHILTGEMVAIKMDKNTLGSDDLPRIKTEALK 62
DB ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
5 DYDELLKYYELHETIGTGFGPAKVKLASHLITGEKVAIKMDKESLGDGLPRVKTEIDAMK 64
QY 63 NLRHQHICOLYHVLETANKIFMWLECYCPGSELDYIISQDRLSEETRVVFRQIVSAVAY 122
DB ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
65 NLSHQHVCRLYHYVETPKKIFMWLECYCPGSELDYIISQDRLSEETRVVFRQIVSAVAY 124
QY 123 VHSQGYAHRDLKPENLDFDEYHKLLIDFGLCAKPKGNKDYHLQTCGSLAYAAPELIQ 182
DB ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
125 IHSQGYAHRDLKPENLIDSDQNLKLTDFGLCAKPKGGLDYHLMTCCGSPAYAAPELIQ 184
QY 183 KSYLGSSEADVWSGILLYLMCGFLPPDDDDNVNVALYKIMRGKYDVPKWLSPSILLQ 242
DB ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
185 KATYIGSEADVWSGVLVLMYALMCGFLPPDDDDNVNVALYKIMRGKYELPKWLSPGVLILLQ 244
QY 243 MLQVDPKRIKSMKNLLNHPIMQDYNYPVEWQSKNPFILHDDDCVTELSVHHRRNQWME 302
DB ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
245 MMQVDPKRIKTVKHLNHPMLMHGYSCEVWQSKYPLGYIDECVTELSVFFYKSRSTTT 304
QY 303 DLISLWQYDHLTATYILLAKKARGKPVRLRLSSPSCGQASATPFTDIDKSNWSLEDVTA 362
DB ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
305 RLISEWSYDHITASYLLLSKSHGKAVRLK-HPLAVGDAQVTSFKELRPKSKLDFEEN 363
QY 363 SDKNVYAGLIDY---DWCEDDLGTGAATPRT-SQFTKYMTESNGVSKSLTPALCRTPAN 418
DB ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
364 GETAYVFGSDFDSDELFLSEDFTISSEFHTPEYVKGRLEFNSVDSAPATPVQNRARH 423
QY 419 KLNKENVYTPKSAVKNSEYFMPPEKTPV--KNQHKREILTPNRYTPPSKARNQCLK 476
DB ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
424 KNEDKENSNT--AVARDENFLHPAWPTPPRRKQNEKKGILTPNK-NTQTEKKQS-K 479
QY 477 ETPIKIPVNSTGTDKLMGTGVIISPERCRSVELDINQAHMEETPKRGAKVFGSLERGLQK 536
DB ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
480 ETPTKKPI---GTGEEFANVISPERCRSVELDINQAHIDSQAOKKGAKVFGSLERGLQK 536
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QY 537 VITVLTRSKRGKSGARDGPRRLKLHLNVTTTRLVNPDQLLNEIMSLPKKHVDVFOVKGYTL 596
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537 MITMLTPSKRGKGYTREGPRKLRAHNVTTTNTVNPQLNQIVRLVPSKXNDVFOVKGYTL 596
QY 597 KCTQSDSGKVTMOFELEVCQLOKDPDVVGIRQRRLKGDWVYKRLVDEDLSSCKV 651
DB ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
597 KCTQSDSGKVTMOFELEVCQLSKSEVVGIRQRRLKGDWVYKRLVDEDLSSCKV 651

RESULT 12
Q5ZL85_CHICK PRELIMINARY; PRT; 657 AA.
AC Q5ZL85;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DE Hypothetical protein.
DE ORFNames=RCMB04_7d18;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
RA Fiedler P., Kutter S., Blagodzinski A., Kostovska D., Koter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursa lymphocytes to facilitate
RT gene function analysis.";
RL Genome Biol. 6:R6-R6(2005).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
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CC -----
DR EMBL; AJ719849; CAG31508.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 657 AA; 74226 MW; 4481FBCBD98C50E8 CRC64;

Query Match 60.4%; Score 2083; DB 2; Length 657;
Best Local Similarity 61.2%; Pred. No. 7.8e-132;
Matches 405; Conservative 94; Mismatches 145; Indels 18; Gaps 7;

QY 1 MKDYDELLKYYELHETIGTGFGPAKVKLACHILTGEMVAIKMDKNTLGSDDLPRIKTEIA 60
DB ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
3 VSDYDELLKYYELHETIGTGFGPAKVKLGHLLTGEKVAIKMDKVALGDDGLPRVKTEIDA 62
QY 61 LKNLRHQHICOLYHVLETANKIFMWLECYCPGSELDYIISQDRLSEETRVVFRQIVSAV 120
DB ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
63 MNLSHQHVCRLYHYVETSKIFMWLVGCPGSELDYIISQDRLSEETRVVFRQIVSAI 122
QY 121 AVHSQGYAHRDLKPENLDFDEYHKLLIDFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180
DB ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
```



```

Db 123 AYVHSQGYAHRDLKPENLLIDEHNLKLIIDFGLCAKPKGGLDYRLNTCCGSPAYAAPELI 182
Qy 181 QGKSYLGSEADVMSGILLVYLMCGFLPFDDDDNMALYKIMRGKYDVPKWLSPSSILL 240
Db 183 QGRAYIGSEADINSMGVLVALLCGFLPFDDDDNMALYRRTIRGKAVPKWLSPSLL 242
Qy 241 QOMLVDPKKRI SMKLNHPWIMODYNYVVEQSKNPPFHLDDDCVTELSVHRRNQ 300
Db 243 NQLQVDPKKRI TVKHLSPWLMQGYSDAVQWQSKYPLGHLDEDCVTELSVPHNSREN 302
Qy 301 MEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSSPCQASATPTDIKSN-WSLED 359
Db 303 ISALISKWYDQWTSATLLQSKKPKRGKRIHLAIPS-QTGHASTQSASIGSEKAMYED 361
Qy 360 V-TASDKNYVAGIDVDMCDDLLSTGAATP-----RTSQTKYWTESNGVESKSLT 409
Db 362 VPDSCVDPDAFGSMWF---SDAASLPESPLEBSFLNTHRTKQHSRHDITQLGDMFEFTLS 418
Qy 410 PALCRTPANKLKNKENYVTPKSAVKNEEYFMPPEKTPVNNKQHKREILTPNRYTTPSK 469
Db 419 PVTRKVASKKHANKENY-DAESALRNLPELPAKPAKSAFSKQTEKQVQGIP--FQAPTS 475
Qy 470 ARNQCLKETPIKIPVNSGTGDKLMTGVI SPERCERSVELDLNOAHMEETPKRGKAVFGS 529
Db 476 KESQFTVTPVKPKPTNTCELTATEVLPEKCHSVLDLNRCHVDSSQKKAKLFGS 535
Qy 530 LERGLDKVITVLTSRKSGSARDGPRRLKLIHYNVTTTTLVNPQLLNEIMSLPKKHVDF 589
Db 536 LERGLDKVITVLTGPKKRSRPGPKLKAHYNVTTTQLLNPQLLNEIISVLSSKKQVEY 595
Qy 590 VQKGYTLKCOQSDPGKVTWQFLEVCOLQKDPVGIIRORLKGDAWYKRLVEDILSSC 649
Db 596 VKKGYTLKCOQDPFGRESKMFLEVCRLSKNGAVGIRQLRGDAWYKRLVEDILSSC 655
Qy 650 KV 651
Db 656 QV 657

RESULT 13
Q7ZN5 BRARE
ID Q7ZN5 BRARE PRELIMINARY; PRT; 676 AA.
AC Q7ZN5
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DE 07-FEB-2006, entry version 19.
DE Similar to maternal embryonic leucine zipper kinase.
GN Name=melk;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Saito R., Watanabe S.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AB108827; BAC75706.1; -; mRNA.
CC HSSP; P49137; 1NY3.
CC ZFIN; ZDB-GENE-990603-5; melk.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.

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DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 676 AA; 76954 MW; 9E24E4B4E8DE5905 CRC64;

Query Match 55.7%; Score 1920; DB 2; Length 676;
Best Local Similarity 57.6%; Pred. No. 8.2e-121;
Matches 392; Conservative 84; Mismatches 150; Indels 54; Gaps 14;

Qy 6 ELKKYELHETIGTGFAKVKLACHILLTGEMVAIKIMDKNTLGLDLPRIKTEALKNLR 65
Db 8 ELKKHYEVYETIGSGGFAKVKLGRHKLGTGEKVAIKIMEKKDGLDDLPVRKIEEAMKNS 67
Qy 66 HQHICOLYHVLETANKIFMVLBYCPGGELFDYIIISODRLSEEBETRVVFRQIVSAVYHS 125
Db 68 HQHVCELHYVETTSKIYVLEVCPPGELFDYIIIAKORLSEEBETRVVFRQIISALAYVHS 127
Qy 126 QGYAHRDLKPENLLFDYHKLKLIIDFGLCAKPKGNKYHLQTCGGSGLAYAAPELIQKSY 185
Db 128 QGYAHRDLKPENLLIDEDHNLKLIIDFGLCAKPKGGLGFELLTCCGSPAYAAPELIQKAY 187
Qy 186 LGSEADVMSGILLVYLMCGFLPFDDDDNMALYKIMRGKYDVPKWLSPSSILLQOMLO 245
Db 188 LGSEADVMSGILLVYLMCGFLPFDDDDNMALYKIMRGKYDVPKWLSPSSILLQOMMQ 247
Qy 246 VDPKRIKIMKLNHPWIMODYNYVVEQSKNPPFHLDDDCVTELSVHRRNQRTMEDLI 305
Db 248 VDPKRLTVKHLDPWNRGYSTPVETHSKYPLGHIDEDCITEMAVTQSKQRTIQLV 307
Qy 306 SLWQYDHLTATYLLLLAKKARGKPVRLR-----LSFSFCQASATPTD--IKSNWLSLED 359
Db 308 SEWKYDQITATYLLLLAKKRGPRVLRACPVDIVC-----SPLQDMQLKKSLLAFTD 362
Qy 360 VTASDKNYVAGIDVDMCDDLLSTGAA-----TPTSQF---TKYWTESNGVESK 406
Db 363 DDGVHPVLGSMVFPDDCYDDDENPMTPLPKNTHNTTNTPRMKLYPETTEKWN-----M 416
Qy 407 SLTPAL-----CRTPAK-----LKNKENYVTPKSAVKNEEYFMPPEKTPV--NKNQHKR 455
Db 417 AYSPIVHSRPRCPKQPERERTKENKENLAVPGT---DGDVLPALPAPRTPTYNRKVKSNR 473
Qy 456 EILTPNRYTTPS-----KARNQCLKETPIKIPVNSTGT---DKLMTGVI SPERRCHSVBL 508
Db 474 TVMTTTPHNHNNKSEVNGKAGSATKEGSRREVEQQOQOQGLNMLAFSPERRSR--L 531
Qy 509 DLNQAHMEETPKRGKAVFGSLERGLDKVITVLTSRKSGSARDGPRRLKLIHYNVTTTL 568
Db 532 DLAGCQVDSGQKRGKAVFGSLERGLDKVITVLTSPKKGK--PRDGPRIKRAQNVNLTNQ 590
Qy 569 VNPDLNLEIMSLPKKHVDFVQKGYTLKCOQSDPGKVTWQFLEVCOLQKDPVVGIRR 628
Db 591 TWADQVLMQILPEKNDVFKQGYTLKCHTQSDFGKVTWQFLEVCOLQKDPVVGIRR 650
Qy 629 QRLKGDWYKRLVEDILSS 648
Db 651 QRLKGDWYKRLVEDILSS 670

RESULT 14
Q7ZU72 BRARE
ID Q7ZU72 BRARE PRELIMINARY; PRT; 676 AA.
AC Q7ZU72
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 22.

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: November 21, 2006, 14:04:10 ; Search time 201 Seconds
(without alignments)
1480.835 Million cell updates/sec

Title: US-10-656-598-2

Perfect score: 3447

Sequence: 1 MKDYDELLKYYELHETIGTG.....KGDWVYKRLVEDILSSCKV 651

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A: Geneseq_8:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*
10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3447	100.0	651	5 AAB47857	Aab47857 KIAA0175
2	3447	100.0	651	6 ABUS6727	Abus6727 Lung canc
3	3447	100.0	651	6 ABUS7635	Abus7635 Different
4	3447	100.0	651	7 ADB80563	Adb80563 Ovarian c
5	3447	100.0	651	7 ADE38347	Ade38347 Human pro
6	3447	100.0	651	7 ADN39188	Adn39188 Cancer/an
7	3447	100.0	651	8 ADM72651	Adm72651 Human TAS
8	3447	100.0	651	8 ADM72217	Adm72217 Human TAS
9	3447	100.0	651	8 ADN06036	Adn06036 Antipsori
10	3447	100.0	651	8 ADQ19625	Adq19625 Human sof
11	3447	100.0	651	8 ADU06466	Adu06466 Novel bro
12	3447	100.0	651	9 ADX07297	Adx07297 Cyclin-de
13	3447	100.0	651	9 ADW93570	Adw93570 Human mat
14	3447	100.0	651	9 ADY15428	Ady15428 PRO poly
15	3447	100.0	651	9 ADY20530	Ady20530 PRO poly
16	3447	100.0	651	9 AEB57148	Aeb57148 Human mat
17	3447	100.0	651	10 AEF71795	Aef71795 Human gen
18	3447	100.0	656	8 ADX91596	Adx91596 Plant ful
19	3447	100.0	656	8 ADX91597	Adx91597 Plant ful
20	3447	100.0	656	8 ADX91598	Adx91598 Plant ful
21	3260.5	94.6	620	8 ABM83187	Abm83187 Human dia
22	3246.5	94.2	628	8 ABM83195	Abm83195 Human dia
23	3216.5	93.3	612	8 ADU66595	Adu66595 Human kin

ALIGNMENTS

RESULT 1

AAB47857

ID AAB47857 standard; protein; 651 AA.

XX AC AAB47857;

XX XX

DT 02-APR-2002 (first entry)

XX XX

DE KIAA0175 protein.

XX XX

KW Antisense; KIAA0175; inhibitor; tumour; P21; P53; chemosensitivity;

KW radiosensitivity; gamma-irradiation; hydroxy urea; cell cycle arrest;

KW sensitization; neoplastic disease; chemotherapy; radiotherapy; cancer.

XX XX

OS Homo sapiens.

XX XX

PN WO200191739-A2.

XX XX

PD 06-DEC-2001.

XX XX

PF 30-MAY-2001; 2001WO-US017644.

XX XX

PR 31-MAY-2000; 2000US-0208435P.

XX XX

PA (CHIR) CHIRON CORP.

XX XX

PI Wu B, Seeley TW, Williams LT;

XX XX

DR WPI; 2002-122034/16.

XX XX

DR N-PSDB; AAI72250.

XX XX

PT New isolated specific inhibitor useful for decreasing the expression of

PT the inhibitor in a mammalian cell.

XX XX

PS Disclosure; Page 57-59; 60pp; English.

XX XX

CC This protein is encoded by the KIAA0175 cDNA. Antisense oligonucleotides

CC were tested to observe their effect on the kinetics of the KIAA0175

CC transcript. Inhibitors of KIAA0175 may be used for decreasing the

CC expression of KIAA0175 in mammalian cell (preferably tumour cell). They

CC may also be used for decreasing the expression of P21 and P53 in a

CC mammalian cell, for increasing the chemosensitivity and/or

CC radiosensitivity of a mammalian cell by measuring a reduction in gamma-

CC irradiation or hydroxy urea induced P53 or P21 protein levels measuring a

CC reduction in gamma-irradiation or hydroxy urea induced cell cycle arrest

CC and measuring an increase in gamma-irradiation or hydroxy urea induced

CC

CC cell sensitization, and for treating neoplastic disease in a mammal. The
CC inhibitor provides beneficial improvement of chemo and/or radiotherapy
CC despite low transfection efficiency (10 - 70%) and/or transient gene
CC expression. The inhibitor decreases the side effects of the cancer
XX therapy
XX
SQ Sequence 651 AA;

Query Match 100.0%; Score 3447; DB 5; Length 651;
Best Local Similarity 100.0%; Pred. No. 1.2e-294;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDYDELLKYYELHETIGTGGAFAKVKLACHILTGEMVAIKIMDKNTLGSGLPRIKTEIEA 60
DB 1 MKDYDELLKYYELHETIGTGGAFAKVKLACHILTGEMVAIKIMDKNTLGSGLPRIKTEIEA 60

QY 61 LKNLRHQHICQLYHVLETANKIFMWLEYPGSGELFDYIISQDRLSEETRVVFRQIVSAV 120
DB 61 LKNLRHQHICQLYHVLETANKIFMWLEYPGSGELFDYIISQDRLSEETRVVFRQIVSAV 120

QY 121 AYVHSQGYAHRDLKPNELLFDEYHKLKLDIFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180
DB 121 AYVHSQGYAHRDLKPNELLFDEYHKLKLDIFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180

QY 181 QGKSYLGSEADVWMSGILLVLMCGFLPFDDNNMALYKKIMRGKYDVPKWLSPSSILL 240
DB 181 QGKSYLGSEADVWMSGILLVLMCGFLPFDDNNMALYKKIMRGKYDVPKWLSPSSILL 240

QY 241 QQMLQVDPKRIISMKNLLNHPIMQDYNYPVEWQSKNPFHLLDDCVTEL SVHHRNROT 300
DB 241 QQMLQVDPKRIISMKNLLNHPIMQDYNYPVEWQSKNPFHLLDDCVTEL SVHHRNROT 300

QY 301 MEDLISLWQYDHLTATYLLLLAKKARGKPVRLSLSFSCQASATPTDIKSNWLSLEDV 360
DB 301 MEDLISLWQYDHLTATYLLLLAKKARGKPVRLSLSFSCQASATPTDIKSNWLSLEDV 360

QY 361 TASDKNVVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
DB 361 TASDKNVVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420

QY 421 KKNENYVTPKSAVKNEEYFMFPPEKTPVNKNQHKREILTPPNRYTTPSKARNQCLKETPI 480
DB 421 KKNENYVTPKSAVKNEEYFMFPPEKTPVNKNQHKREILTPPNRYTTPSKARNQCLKETPI 480

QY 481 KIPVNSTGTDLMTGVTSPERRCRSVELDLNQAHMEETPKKCAKVGSLERGLDKVITV 540
DB 481 KIPVNSTGTDLMTGVTSPERRCRSVELDLNQAHMEETPKKCAKVGSLERGLDKVITV 540

QY 541 LTRSKRKGSGARDGPRRLKLYHNTVTRLVNPDQLLNEIMSILPKGKHVDVFQKGTYLKCQT 600
DB 541 LTRSKRKGSGARDGPRRLKLYHNTVTRLVNPDQLLNEIMSILPKGKHVDVFQKGTYLKCQT 600

QY 601 QSDFGKVTMQFELEVQOLQKPDVVGIRRLKGDGAWYKRLVEDILSSCKV 651
DB 601 QSDFGKVTMQFELEVQOLQKPDVVGIRRLKGDGAWYKRLVEDILSSCKV 651

RESULT 2
ABU56727
ID ABU56727 standard; protein; 651 AA.
AC ABU56727;
XX
XX 02-APR-2003 (first entry)
DE Lung cancer-associated polypeptide #320.
XX
XX Lung cancer-associated polypeptide; cytostatic; emphysema;
XX antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
XX small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX

OS Unidentified.
XX
PN WO200286443-A2.
XX
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US012476.
XX
PF 18-APR-2001; 2001US-0284770P.
PR 18-MAY-2001; 2001US-0290492P.
PR 09-NOV-2001; 2001US-0332449P.
PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334370P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
DR WPI; 2003-093161/08.
DR N-PSDB; ABX76456.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
PS Claim 27; Page 436; 453pp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABU56408-ABU56745 represent lung cancer-associated polypeptides of the
CC invention
XX
SQ Sequence 651 AA;

Query Match 100.0%; Score 3447; DB 6; Length 651;
Best Local Similarity 100.0%; Pred. No. 1.2e-294;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDYDELLKYYELHETIGTGGAFAKVKLACHILTGEMVAIKIMDKNTLGSGLPRIKTEIEA 60
DB 1 MKDYDELLKYYELHETIGTGGAFAKVKLACHILTGEMVAIKIMDKNTLGSGLPRIKTEIEA 60

QY 61 LKNLRHQHICQLYHVLETANKIFMWLEYPGSGELFDYIISQDRLSEETRVVFRQIVSAV 120
DB 61 LKNLRHQHICQLYHVLETANKIFMWLEYPGSGELFDYIISQDRLSEETRVVFRQIVSAV 120

QY 121 AYVHSQGYAHRDLKPNELLFDEYHKLKLDIFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180
DB 121 AYVHSQGYAHRDLKPNELLFDEYHKLKLDIFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180

QY 181 QGKSYLGSEADVWMSGILLVLMCGFLPFDDNNMALYKKIMRGKYDVPKWLSPSSILL 240
DB 181 QGKSYLGSEADVWMSGILLVLMCGFLPFDDNNMALYKKIMRGKYDVPKWLSPSSILL 240

QY 241 QQMLQVDPKRIISMKNLLNHPIMQDYNYPVEWQSKNPFHLLDDCVTEL SVHHRNROT 300
DB 241 QQMLQVDPKRIISMKNLLNHPIMQDYNYPVEWQSKNPFHLLDDCVTEL SVHHRNROT 300

Db 241 QOMLQVDPKRI:SMKULLNHPIMQDYNYPVWQSKNPFILHDDDCVTELSVHHRNQT 300
Qy 301 MEDLISLWQYDHLTATYLLALLAKARGKPVRLRLSFSFGQASATPFTDIKSNWNSLEDV 360
Db 301 MEDLISLWQYDHLTATYLLALLAKARGKPVRLRLSFSFGQASATPFTDIKSNWNSLEDV 360
Qy 361 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSFTKYWTESNGVESKSLTPALCRTPANKL 420
Db 361 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSFTKYWTESNGVESKSLTPALCRTPANKL 420
Qy 421 KKNENYVTPKSAVQNEEYFMPPEKTPVKNQKHREILLTPNRYTTPSKARNOCLKETPI 480
Db 421 KKNENYVTPKSAVQNEEYFMPPEKTPVKNQKHREILLTPNRYTTPSKARNOCLKETPI 480
Qy 481 KIPVNSTGTDKMTGTVISPERCRSVELDLNQAHEETPKRGAKVFGSLERGLDKVITV 540
Db 481 KIPVNSTGTDKMTGTVISPERCRSVELDLNQAHEETPKRGAKVFGSLERGLDKVITV 540
Qy 541 LTRSKRKSARDGPRRLKLYNVTTRLVNPDQLLINEIMSLPKKHVDVQKGYTLKQOT 600
Db 541 LTRSKRKSARDGPRRLKLYNVTTRLVNPDQLLINEIMSLPKKHVDVQKGYTLKQOT 600
Qy 601 QSDFGKVTMQFELEVCQKQPDVVGIRROKLGDAWYKRLVEDILSSCKV 651
Db 601 QSDFGKVTMQFELEVCQKQPDVVGIRROKLGDAWYKRLVEDILSSCKV 651

RESULT 3

ABUS7635
ID ABUS7635 standard; protein; 651 AA.
AC ABUS7635;

09-APR-2003 (first entry)

Differentially expressed breast cancer associated protein #22.

Breast cancer; differential gene expression; BC-cDNA;
breast cancer diagnosis; breast cancer monitoring;
breast cancer treatment; breast cancer staging.

OS Homo sapiens.

US2002156263-A1.

24-OCT-2002.

04-OCT-2001; 2001US-00974298.

05-OCT-2000; 2000US-0238331P.

(CHEN/) CHEN H.

Chen H;

WPI; 2003-182653/18.

New cDNAs, which are differentially expressed in (metastatic) breast cancer useful for diagnosing or staging, breast cancer, or for monitoring the treatment of breast cancer in an individual.

Example; SEQ ID NO 112; 30pp; English.

The invention describes a combination of cDNAs (designated BC-cDNAs), which are differentially expressed in breast cancer. The combination includes 152 cDNA sequences, or their complements. The protein encoded by any of these BC-cDNAs is useful for screening several molecules or compounds to identify at least one ligand that specifically binds the protein, producing or preparing polyclonal or monoclonal antibodies, or purifying antibodies from a sample. The antibodies, which specifically bind the protein differentially expressed in breast cancer is useful for detecting the expression of a protein in a sample. The BC-cDNAs are also useful for diagnosing, monitoring the treatment of, or staging, breast

CC cancer. This is the amino acid sequence of a differentially expressed breast cancer associated protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at seqdata.uspto.gov/sequence.html?DocID=20020156263

XX Sequence 651 AA;

Query Match 100.0%; Score 3447; DB 6; Length 651;
Best Local Similarity 100.0%; Pred. No. 1.2e-294;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKDYDELLKYVELHETICTGGFAKVKLACHILTGEWVAIKMDKNTLSGDLPRIKTEIEA 60
Db 1 MKDYDELLKYVELHETICTGGFAKVKLACHILTGEWVAIKMDKNTLSGDLPRIKTEIEA 60
Qy 61 LKNLRHQHICQLYHVLETPANKIFWVLEYCPGGELFDYIISQDRLESEETRVVFRQIVSAV 120
Db 61 LKNLRHQHICQLYHVLETPANKIFWVLEYCPGGELFDYIISQDRLESEETRVVFRQIVSAV 120
Qy 121 AYVHSQGYAHRDLKPENLLFDEYHKLKIDFGLCAKPKGNKYHLYQTCGSLAYAAPALI 180
Db 121 AYVHSQGYAHRDLKPENLLFDEYHKLKIDFGLCAKPKGNKYHLYQTCGSLAYAAPALI 180
Qy 181 QKSYLGSSEADVWSMGILLYVLMCGFLPFDDNNWALYKKIMRGKYDVPKWLSPSSILL 240
Db 181 QKSYLGSSEADVWSMGILLYVLMCGFLPFDDNNWALYKKIMRGKYDVPKWLSPSSILL 240
Qy 241 QOMLQVDPKRI:SMKULLNHPIMQDYNYPVWQSKNPFILHDDDCVTELSVHHRNQT 300
Db 241 QOMLQVDPKRI:SMKULLNHPIMQDYNYPVWQSKNPFILHDDDCVTELSVHHRNQT 300
Qy 301 MEDLISLWQYDHLTATYLLALLAKARGKPVRLRLSFSFGQASATPFTDIKSNWNSLEDV 360
Db 301 MEDLISLWQYDHLTATYLLALLAKARGKPVRLRLSFSFGQASATPFTDIKSNWNSLEDV 360
Qy 361 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSFTKYWTESNGVESKSLTPALCRTPANKL 420
Db 361 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSFTKYWTESNGVESKSLTPALCRTPANKL 420
Qy 421 KKNENYVTPKSAVQNEEYFMPPEKTPVKNQKHREILLTPNRYTTPSKARNOCLKETPI 480
Db 421 KKNENYVTPKSAVQNEEYFMPPEKTPVKNQKHREILLTPNRYTTPSKARNOCLKETPI 480
Qy 481 KIPVNSTGTDKMTGTVISPERCRSVELDLNQAHEETPKRGAKVFGSLERGLDKVITV 540
Db 481 KIPVNSTGTDKMTGTVISPERCRSVELDLNQAHEETPKRGAKVFGSLERGLDKVITV 540
Qy 541 LTRSKRKSARDGPRRLKLYNVTTRLVNPDQLLINEIMSLPKKHVDVQKGYTLKQOT 600
Db 541 LTRSKRKSARDGPRRLKLYNVTTRLVNPDQLLINEIMSLPKKHVDVQKGYTLKQOT 600
Qy 601 QSDFGKVTMQFELEVCQKQPDVVGIRROKLGDAWYKRLVEDILSSCKV 651
Db 601 QSDFGKVTMQFELEVCQKQPDVVGIRROKLGDAWYKRLVEDILSSCKV 651

RESULT 4

ADB80563

ID ADB80563 standard; protein; 651 AA.

XX ADB80563;

04-DEC-2003 (first entry)

Ovarian cancer-associated protein #64.

cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis;
post-operative chemotherapy; radiation therapy; tumour prognosis;
pre-cancerous lesion detection.

OS Homo sapiens.

XX

PN W02002102235-A2.
XX 27-DEC-2002.
XX 18-JUN-2002; 2002WO-US019297.
XX 18-JUN-2001; 2001US-0299234P.
PR 27-AUG-2001; 2001US-0315287P.
PR 05-SEP-2001; 2001US-0317544P.
PR 13-NOV-2001; 2001US-0350666P.
PR 12-APR-2002; 2002US-0372246P.
XX (EOS-) EOS BIOTECHNOLOGY INC.
XX Mack DH, Gish KC;
PI WPI; 2003-167431/16.
DR N-PSDB; ADB80562.
XX Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
XX Claim 13; Page 319; 332pp; English.
XX The invention relates to a method of detecting an ovarian cancer-associated transcript in a cell from a patient, by contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to any of one of 80 nucleic acid sequences given in the specification. The method is useful in diagnosing ovarian cancer and in identifying and using agents and/or targets that inhibit ovarian cancer. The nucleic acid molecule, polypeptide and the antibody may also be used in detecting ovarian cancers, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting patients for post-operative chemotherapy or radiation therapy, in selecting mode of therapy, determining tumour prognosis, early detection of pre-cancerous lesions, and as vaccines. This sequence corresponds to one of the proteins used for the detection method of the invention.
XX Sequence 651 AA;
Query Match 100.0%; Score 3447; DB 7; Length 651;
Best Local Similarity 100.0%; Pred. No. 1.2e-294;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKDYDELLKYYELHETIGTGGAFAKVLACHILTGEMVAIKMDKNTLGSDDLPRIKTEISA 60
DB 1 MKDYDELLKYYELHETIGTGGAFAKVLACHILTGEMVAIKMDKNTLGSDDLPRIKTEISA 60
QY 61 LKNLRHQHICQLYHVLETANKIFWVLEYCPGGELEFDYIISODRLSEETRVVPRQIVSAV 120
DB 61 LKNLRHQHICQLYHVLETANKIFWVLEYCPGGELEFDYIISODRLSEETRVVPRQIVSAV 120
QY 121 AYVHSQGYAHRDLKPNELLFDEYHKLKIDFGLCAKPKGNKYHLQTCGSLAYAAPELI 180
DB 121 AYVHSQGYAHRDLKPNELLFDEYHKLKIDFGLCAKPKGNKYHLQTCGSLAYAAPELI 180
QY 181 QGKSYLGSEADVMSGILLVYLMCGFLPFDDNNMALYKKIMRGKYDVPKWSPPSILL 240
DB 181 QGKSYLGSEADVMSGILLVYLMCGFLPFDDNNMALYKKIMRGKYDVPKWSPPSILL 240
QY 241 QOMLVDPKRIKSMKLNHPWIMQDYNYPVEWQSKNPFTHLDDCCVTELSVHHRNROT 300
DB 241 QOMLVDPKRIKSMKLNHPWIMQDYNYPVEWQSKNPFTHLDDCCVTELSVHHRNROT 300
QY 301 MEDLISLMQYDHLTATYLLLLAKKARGKPVRLRLSPSCQASATPFTDIKSNWNSLEDV 360
DB 301 MEDLISLMQYDHLTATYLLLLAKKARGKPVRLRLSPSCQASATPFTDIKSNWNSLEDV 360
QY 361 TASDKNYPVAGLIIDYDWCEDDLSTGAATPRTSQTKYWTESNGVESKSLTPALCRTPANKL 420
DB 361 TASDKNYPVAGLIIDYDWCEDDLSTGAATPRTSQTKYWTESNGVESKSLTPALCRTPANKL 420

QY 421 KKNENVYTPKSAVKNEEYFMPEPKTPVKNQKHKEILTPNRYTPPSKARNQCLKETPI 480
DB 421 KKNENVYTPKSAVKNEEYFMPEPKTPVKNQKHKEILTPNRYTPPSKARNQCLKETPI 480
QY 481 KIPVNSTGTDKLMTGVIISPERRCRSVELDLNQAHMEETPKRGAKVFGSLERGLDKVITV 540
DB 481 KIPVNSTGTDKLMTGVIISPERRCRSVELDLNQAHMEETPKRGAKVFGSLERGLDKVITV 540
QY 541 LTRSKRKGSGARDGPRRLKLYHNVTTTRLVNPDQLNEIWSILPKKHVDVFOKGYTLKCO 600
DB 541 LTRSKRKGSGARDGPRRLKLYHNVTTTRLVNPDQLNEIWSILPKKHVDVFOKGYTLKCO 600
QY 601 QSDFGKVTMQFEVLCQKPDVVGIRQRKLGDAWVYKRLVEDILSSCKV 651
DB 601 QSDFGKVTMQFEVLCQKPDVVGIRQRKLGDAWVYKRLVEDILSSCKV 651
RESULT 5
ADE38347
ID ADE38347 standard; protein; 651 AA.
XX ADE38347;
XX 29-JAN-2004 (first entry)
XX Human protein 2089 amino acid sequence.
XX tumorigenic disorder; angiogenic disorder; aberrant gene expression;
XX aberrant protein activity; cytostatic; antithyroid; antidiabetic;
KW ophthalmological; cancer; breast cancer; colon cancer; lung cancer;
KW prostatic cancer; Grave's disease; diabetic retinopathy; protein 2089.
XX Homo sapiens.
OS WO2003065006-A2.
XX 07-AUG-2003.
XX 30-JAN-2003; 2003WO-US002588.
XX 31-JAN-2002; 2002US-0353600P.
PR 15-MAR-2002; 2002US-0364517P.
PR 09-APR-2002; 2002US-0371075P.
PR 10-APR-2002; 2002US-0371507P.
PR 16-APR-2002; 2002US-0372984P.
PR 19-APR-2002; 2002US-0374194P.
PR 24-MAY-2002; 2002US-0382995P.
PR 31-MAY-2002; 2002US-0385023P.
PR 14-JUN-2002; 2002US-0388533P.
PR 17-JUN-2002; 2002US-0389395P.
PR 25-JUN-2002; 2002US-0391324P.
PR 15-JUL-2002; 2002US-0395944P.
PR 22-JUL-2002; 2002US-0397726P.
PR 13-AUG-2002; 2002US-0403046P.
PR 22-AUG-2002; 2002US-0405155P.
PR 27-AUG-2002; 2002US-0406361P.
PR 25-OCT-2002; 2002US-0421195P.
PR 12-NOV-2002; 2002US-0425456P.
PR 19-NOV-2002; 2002US-0427626P.
PR 10-DEC-2002; 2002US-0432122P.
XX (MILL-) MILLENNIUM PHARM INC.
PA Hunter JJ, Macbeth KJ, Tsai F, Lesoon A, Lightcap ES;
XX Williamson MW, Rudolph-Owen LA;
PI WPI; 2003-646176/61.
XX N-PSDB; ADE38346.
XX Treating subject having tumorigenic disorder or angiogenic disorder caused by aberrant polypeptide e.g., N-formylpeptide receptor or nucleic acid, by administering a modulator.

XX	PS	Disclosure; SEQ ID NO 8; 454pp; English.
XX	CC	This invention relates to a novel method of treating a human subject
CC	CC	having a tumorigenic disorder or angiogenic disorder, caused by aberrant
CC	CC	gene expression or activity of an isolated protein, by administering a
CC	CC	modulator. The modulator may have cytostatic, antithyroid, antidiabetic
CC	CC	or ophthalmological activity. The method is useful for treating a subject
CC	CC	having a tumorigenic or angiogenic disorder, in particular for treating
CC	CC	cancer (for example breast cancer, colon cancer, lung cancer or prostatic
CC	CC	cancer) and, for example, Grave's disease and diabetic retinopathy. The
CC	CC	present sequence is the amino acid sequence of the novel isolated human
CC	CC	protein 2089 of the invention.
XX	XX	Sequence 651 AA;
XX	XX	Query Match 100.0%; Score 3447; DB 7; Length 651;
XX	XX	Best Local Similarity 100.0%; Pred. No. 1.2e-294;
XX	XX	Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MKDYDELLKYYELHETIGTGGAFAKVKLACHILTGEMVAIKIMDKNTLGSGLPRIKTEIEA 60
DB	1	MKDYDELLKYYELHETIGTGGAFAKVKLACHILTGEMVAIKIMDKNTLGSGLPRIKTEIEA 60
QY	61	LKULRHQHICOLYHVLETANKIPMWLEYCPGGELFDYIISQRLSEETRVVFRQIVSAV 120
DB	61	LKULRHQHICOLYHVLETANKIPMWLEYCPGGELFDYIISQRLSEETRVVFRQIVSAV 120
QY	121	AVVHSGYAHARDLKPENLAFDEYHKLKIDFGLCAPKGNKDVLQTCGSLAYAAPELI 180
DB	121	AVVHSGYAHARDLKPENLAFDEYHKLKIDFGLCAPKGNKDVLQTCGSLAYAAPELI 180
QY	181	QKSYLGSSEADVMSGILLYVLMCGFLPDDDDNMALYKKIMRGKYDVPKWLPSSILL 240
DB	181	QKSYLGSSEADVMSGILLYVLMCGFLPDDDDNMALYKKIMRGKYDVPKWLPSSILL 240
QY	241	QOMLQVDPKRSIMKNLHNPWTMODYNYPVVEHQSNPFIHLDDDCVTELSVHHRNQT 300
DB	241	QOMLQVDPKRSIMKNLHNPWTMODYNYPVVEHQSNPFIHLDDDCVTELSVHHRNQT 300
QY	301	MEDLISLWQYDHLTATYLLALLAKARGKPVRLRLSSFCGQASATPFTDIKNNWSLEDV 360
DB	301	MEDLISLWQYDHLTATYLLALLAKARGKPVRLRLSSFCGQASATPFTDIKNNWSLEDV 360
QY	361	TASDKNYVAGLDYDWCEDDLSTGAATPRTSQTKYWTESNGVESKSLTPALCRTPANKL 420
DB	361	TASDKNYVAGLDYDWCEDDLSTGAATPRTSQTKYWTESNGVESKSLTPALCRTPANKL 420
QY	421	KKENYVTPKSAVKNBEYFMPPEPKTPVNKNQHKREILTPNRYTTPSKARNOCLKETPI 480
DB	421	KKENYVTPKSAVKNBEYFMPPEPKTPVNKNQHKREILTPNRYTTPSKARNOCLKETPI 480
QY	481	KIPVNSTGDKLMTGTVISERRCRSVELDLNOAHMEETPKRGAKVFGSLERGLDKVITV 540
DB	481	KIPVNSTGDKLMTGTVISERRCRSVELDLNOAHMEETPKRGAKVFGSLERGLDKVITV 540
QY	541	LTRSEKSGARDGPRRLKHLHYNTVTRLVNPDQLNEIMSILPKKHVDVQVQGYTLKCO 600
DB	541	LTRSEKSGARDGPRRLKHLHYNTVTRLVNPDQLNEIMSILPKKHVDVQVQGYTLKCO 600
QY	601	QSDFGKVTMQFELEVQOLQKPDVVGIRRLRGDAMVYKRLVEDILSSCKV 651
DB	601	QSDFGKVTMQFELEVQOLQKPDVVGIRRLRGDAMVYKRLVEDILSSCKV 651
XX	XX	RESULT 6
XX	XX	ADN39188
XX	XX	ID ADN39188 standard; protein; 651 AA.
XX	XX	AC ADN39188;
XX	XX	DT 17-JUN-2004 (first entry)
XX	XX	XX

DE	XX	Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:506.
XX	XX	Human; differential expression; cancer; angiogenic disorder;
KW	KW	fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW	KW	inflammatory disease; autoimmune disease;
KW	KW	retinal neovascularisation syndrome; scarring; uterine fibroid;
KW	KW	detection; diagnosis; prognosis; drug screening; drug targeting;
KW	KW	wound healing; contraception; cytostatic; cardiant; immunomodulatory;
XX	XX	vulnary; gene therapy; vaccine.
OS	OS	Homo sapiens.
XX	XX	WO2003042661-A2.
PN	PN	22-MAY-2003.
XX	XX	13-NOV-2002; 2002WO-US036810.
PF	PF	13-NOV-2001; 2001US-0350666P.
XX	XX	21-NOV-2001; 2001US-0332464P.
PR	PR	29-NOV-2001; 2001US-0334393P.
PR	PR	03-DEC-2001; 2001US-0335394P.
PR	PR	14-DEC-2001; 2001US-0340376P.
PR	PR	08-JAN-2002; 2002US-0347211P.
PR	PR	10-JAN-2002; 2002US-0347349P.
PR	PR	08-FEB-2002; 2002US-0355250P.
PR	PR	13-FEB-2002; 2002US-0356714P.
PR	PR	20-FEB-2002; 2002US-0359077P.
PR	PR	29-MAR-2002; 2002US-0368809P.
PR	PR	04-APR-2002; 2002US-0370110P.
PR	PR	12-APR-2002; 2002US-0372246P.
PR	PR	05-JUN-2002; 2002US-0386614P.
PR	PR	16-JUL-2002; 2002US-0396839P.
PR	PR	22-JUL-2002; 2002US-039775P.
PR	PR	22-JUL-2002; 2002US-0397845P.
PR	PR	09-SEP-2002; 2002US-0409450P.
XX	XX	(EOSB-) EOS BIOTECHNOLOGY INC.
PA	PA	Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
PI	PI	Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX	XX	WPI; 2003-468649/44.
DR	DR	N-PSDB; ADN39187.
XX	XX	Determining the presence or absence of a pathological cell in a patient,
PT	PT	useful for diagnosing, prognosing or treating cancer, comprises detecting
PT	PT	a nucleic acid in a biological sample.
XX	XX	Claim 12; SEQ ID NO 506; 1385pp; English.
PS	PS	The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC	CC	whose expression is upregulated or downregulated in specific cancers or
CC	CC	other diseases such as angiogenic or fibrotic disorders, and to methods
CC	CC	of determining the presence or absence of a pathological cell in a
CC	CC	patient by detecting a nucleic acid at least 80% identical to those of
CC	CC	the invention or by detecting a polypeptide of the invention. The
CC	CC	invention also relates to expression vectors and host cells comprising a
CC	CC	nucleic acid of the invention; antibodies which specifically bind a
CC	CC	polypeptide of the invention; use of such antibodies for drug targeting;
CC	CC	and methods of screening for modulators of activity or expression of the
CC	CC	polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC	CC	antibodies and methods are useful for diagnosing, prognosing and treating
CC	CC	cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC	CC	atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC	CC	neovascularisation syndromes, scarring, and uterine fibroids. They may
CC	CC	also be useful in wound healing and in contraception. The present
CC	CC	sequence represents a polypeptide of the invention.
XX	XX	Sequence 651 AA;
XX	XX	Query Match 100.0%; Score 3447; DB 7; Length 651;
XX	XX	Best Local Similarity 100.0%; Pred. No. 1.2e-294;

Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDYDELLKYYELHETIGTGGFAKVKLACHILTGEMVAIKIMDKNTLGSDDLPRIKTEIEA 60
DB 1 MKDYDELLKYYELHETIGTGGFAKVKLACHILTGEMVAIKIMDKNTLGSDDLPRIKTEIEA 60

QY 61 LKNLRHQHICQLYHVLLETANKIFMWLEPCPGELFDYIISQDRLSEETRVVFRQIVSAV 120
DB 61 LKNLRHQHICQLYHVLLETANKIFMWLEPCPGELFDYIISQDRLSEETRVVFRQIVSAV 120

QY 121 AYVHSQGYAHRDLKPNELLFDEYHKLIDFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180
DB 121 AYVHSQGYAHRDLKPNELLFDEYHKLIDFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180

QY 181 QGKSYLGSEADVWSMGILLVYLMCGFLPDDNNMALYKIMRGKYDVPKWLSPSSILL 240
DB 181 QGKSYLGSEADVWSMGILLVYLMCGFLPDDNNMALYKIMRGKYDVPKWLSPSSILL 240

QY 241 QQMLQVDPKKRISMKNLLNHPIMQDYNYPVEWQSKNPFILHDDDCVTLSVHHRNROT 300
DB 241 QQMLQVDPKKRISMKNLLNHPIMQDYNYPVEWQSKNPFILHDDDCVTLSVHHRNROT 300

QY 301 MEDLISLMQYDHLTATYLLLLAKKARGKPVRLRLSLFSFCQASATPFTDIKSNWLSLEV 360
DB 301 MEDLISLMQYDHLTATYLLLLAKKARGKPVRLRLSLFSFCQASATPFTDIKSNWLSLEV 360

QY 361 TASDKNYYAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
DB 361 TASDKNYYAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420

QY 421 KKNENYVTPKSAVKNEEYFMFPPEKTPVNKNQHKREILTPNRYTTPSKARNOCLKETPI 480
DB 421 KKNENYVTPKSAVKNEEYFMFPPEKTPVNKNQHKREILTPNRYTTPSKARNOCLKETPI 480

QY 481 KIPVNSTGDKLMTGVI SPERRCRSVELDLNQAHEETPKRGAKVFGSLERGLDKVITV 540
DB 481 KIPVNSTGDKLMTGVI SPERRCRSVELDLNQAHEETPKRGAKVFGSLERGLDKVITV 540

QY 541 LTRSKRKGSAARDGPRRLKHLHYNTTTLVNPOLLNEIMSLPKKHVDVFQKGYTLKCCOT 600
DB 541 LTRSKRKGSAARDGPRRLKHLHYNTTTLVNPOLLNEIMSLPKKHVDVFQKGYTLKCCOT 600

QY 601 QSDFGKVTMQFLEVCQLQKPDVVGIRRORLKGDAWVYKRLVEDILSSCKV 651
DB 601 QSDFGKVTMQFLEVCQLQKPDVVGIRRORLKGDAWVYKRLVEDILSSCKV 651

RESULT 7
ADM72651
ID ADM72651 standard; protein; 651 AA.
XX AC ADM72651;
XX XX
XX 17-JUN-2004 (first entry)
XX DE Human TASK110 polypeptide (clone DNA255289).
XX XX
XX KW TASK; tumour-associated kinase; cytostatic; tumour;
XX KW cell proliferative disorder; cancer; transgenic;
XX KW chromosome identification; tissue typing; human; TASK110; enzyme.
XX OS Homo sapiens.
XX XX
XX PN WO2004024063-A2.
XX XX
XX PD 25-MAR-2004.
XX PF 05-SEP-2003; 2003WO-US027886.
XX PR 11-SEP-2002; 2002US-0410166P.
XX XX
XX PA (GETH) GENENTECH INC.

PI Davis DF, Desauvage FJ, Wood WI, Zhang Z;
XX WPI: 2004-282984/26.
DR N-PSDB; ADM72650.
XX
PT New tumor-associated kinase nucleic acids and polypeptides, useful as
PT hybridization probes for isolating full length TASK DNA, for generating
PT transgenic animals, in chromosome identification, or for tissue typing.
XX
PS Claim 11; Fig 2; 140pp; English.
XX
CC The invention relates to tumour-associated kinase (TASK) polypeptides
CC (II) and encoding polynucleotides. An antibody, oligopeptide (sRNA) or
CC organic molecule that binds to (II) is useful for treating a mammal
CC having a tumour comprising cells expressing (II). Antagonists of TASK are
CC useful for treating or preventing a cell proliferative disorder (e.g.
CC cancer) associated with increased expression or activity of (II). The
CC TASK polynucleotides and polypeptides may be used as hybridization probes
CC for isolating full length TASK DNA, for generating transgenic animals, in
CC chromosome identification, or for tissue typing. The present sequence
CC represents a human TASK110 polypeptide.
SQ Sequence 651 AA;
Query Match 100.0%; Score 3447; DB 8; Length 651;
Best Local Similarity 100.0%; Pred. No. 1.2e-294;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDYDELLKYYELHETIGTGGFAKVKLACHILTGEMVAIKIMDKNTLGSDDLPRIKTEIEA 60
DB 1 MKDYDELLKYYELHETIGTGGFAKVKLACHILTGEMVAIKIMDKNTLGSDDLPRIKTEIEA 60

QY 61 LKNLRHQHICQLYHVLLETANKIFMWLEPCPGELFDYIISQDRLSEETRVVFRQIVSAV 120
DB 61 LKNLRHQHICQLYHVLLETANKIFMWLEPCPGELFDYIISQDRLSEETRVVFRQIVSAV 120

QY 121 AYVHSQGYAHRDLKPNELLFDEYHKLIDFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180
DB 121 AYVHSQGYAHRDLKPNELLFDEYHKLIDFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180

QY 181 QGKSYLGSEADVWSMGILLVYLMCGFLPDDNNMALYKIMRGKYDVPKWLSPSSILL 240
DB 181 QGKSYLGSEADVWSMGILLVYLMCGFLPDDNNMALYKIMRGKYDVPKWLSPSSILL 240

QY 241 QQMLQVDPKKRISMKNLLNHPIMQDYNYPVEWQSKNPFILHDDDCVTLSVHHRNROT 300
DB 241 QQMLQVDPKKRISMKNLLNHPIMQDYNYPVEWQSKNPFILHDDDCVTLSVHHRNROT 300

QY 301 MEDLISLMQYDHLTATYLLLLAKKARGKPVRLRLSLFSFCQASATPFTDIKSNWLSLEV 360
DB 301 MEDLISLMQYDHLTATYLLLLAKKARGKPVRLRLSLFSFCQASATPFTDIKSNWLSLEV 360

QY 361 TASDKNYYAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
DB 361 TASDKNYYAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420

QY 421 KKNENYVTPKSAVKNEEYFMFPPEKTPVNKNQHKREILTPNRYTTPSKARNOCLKETPI 480
DB 421 KKNENYVTPKSAVKNEEYFMFPPEKTPVNKNQHKREILTPNRYTTPSKARNOCLKETPI 480

QY 481 KIPVNSTGDKLMTGVI SPERRCRSVELDLNQAHEETPKRGAKVFGSLERGLDKVITV 540
DB 481 KIPVNSTGDKLMTGVI SPERRCRSVELDLNQAHEETPKRGAKVFGSLERGLDKVITV 540

QY 541 LTRSKRKGSAARDGPRRLKHLHYNTTTLVNPOLLNEIMSLPKKHVDVFQKGYTLKCCOT 600
DB 541 LTRSKRKGSAARDGPRRLKHLHYNTTTLVNPOLLNEIMSLPKKHVDVFQKGYTLKCCOT 600

QY 601 QSDFGKVTMQFLEVCQLQKPDVVGIRRORLKGDAWVYKRLVEDILSSCKV 651
DB 601 QSDFGKVTMQFLEVCQLQKPDVVGIRRORLKGDAWVYKRLVEDILSSCKV 651

RESULT 8

ADMT2217
 ID ADM72217 standard; protein; 651 AA.
 XX AC
 ADM72217;
 XX DT 17-JUN-2004 (first entry)
 XX DE Human TASK110 polypeptide.
 XX TASK; tumour-associated kinase; cytostatic; tumour antigen;
 KW cell proliferative disorder; cancer; transgenic; human.
 XX OS Homo sapiens.
 XX PN WO2004024064-A2.
 XX PD 25-MAR-2004.
 XX PF 05-SEP-2003; 2003WO-US027894.
 XX PR 11-SEP-2002; 2002US-0410166P.
 XX PA (GETH) GENENTECH INC.
 XX PI Desauvage FJ, Wood WI, Zhang Z;
 XX WPI; 2004-282985/26.
 XX DR N-PSDB; ADM72216.
 XX PT New tumor-associated kinase nucleic acids and polypeptides, useful as
 PT hybridization probes for isolating full length TASK DNA, for generating
 PT transgenic animals, in chromosome identification, or for tissue typing.
 XX PS Claim 12; SEQ ID NO 22; 163pp; English.
 XX CC The invention relates to new isolated tumour-associated kinase (TASK)
 CC nucleic acid molecules and encoded polypeptides. Cytostatic. The
 CC antibody, oligopeptide or organic molecule that binds to the TASK
 CC polypeptide are useful for treating a mammal having a tumour comprising
 CC cells expressing the polypeptide. Antagonists of TASK are useful for
 CC treating or preventing a cell proliferative disorder (e.g. cancer)
 CC associated with increased expression or activity of TASK polypeptide. The
 CC TASK polynucleotides and polypeptides may be used as hybridization probes
 CC for isolating full length TASK DNA, for generating transgenic animals, in
 CC chromosome identification, or for tissue typing. The present sequence
 CC represents a human TASK polypeptide.
 XX Sequence 651 AA;
 SQ

Query Match 100.0%; Score 3447; DB 8; Length 651;
 Best Local Similarity 100.0%; Pred. No. 1.2e-294;
 Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDYDELLKYELHETIGTGFPKAVKVLACHILTGEMVAIKMDKNTLGSGLPRIKTEIA 60
 DB 1 MKDYDELLKYELHETIGTGFPKAVKVLACHILTGEMVAIKMDKNTLGSGLPRIKTEIA 60
 QY 61 LKNLRHQHICOLYHVLETANKIFMWLEYCPGGELFDYIISQDRLSEETRVVFRQIVSAV 120
 DB 61 LKNLRHQHICOLYHVLETANKIFMWLEYCPGGELFDYIISQDRLSEETRVVFRQIVSAV 120
 QY 121 AYVHSGYAHRLDKPENLAFDEYHKLKLDIFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180
 DB 121 AYVHSGYAHRLDKPENLAFDEYHKLKLDIFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180
 QY 181 QGKSYLGSBADVWMSGILLYVLMCGFLPFDDNNVMALYKIMRGKYDVPKWLSPSSILL 240
 DB 181 QGKSYLGSBADVWMSGILLYVLMCGFLPFDDNNVMALYKIMRGKYDVPKWLSPSSILL 240
 QY 241 QOMLQVDPKKRISMKULLNHPIMQDYNYPVEWQSKNPFILHDDDCVTELSVHHRNROT 300
 DB 241 QOMLQVDPKKRISMKULLNHPIMQDYNYPVEWQSKNPFILHDDDCVTELSVHHRNROT 300

QY 301 MEDLISLWQYDHLTATYLLLLAKARGKPVRLRLSSFCQASATPPTDIKSNWSLEDV 360
 DB 301 MEDLISLWQYDHLTATYLLLLAKARGKPVRLRLSSFCQASATPPTDIKSNWSLEDV 360
 QY 361 TASDKNYVAGLIDYDKCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
 DB 361 TASDKNYVAGLIDYDKCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
 QY 421 KKNENYVTPKSAVKNEEYFMFPPEKTPVNKNQKHREILTPNNRYTTPSKARNQCLKETPI 480
 DB 421 KKNENYVTPKSAVKNEEYFMFPPEKTPVNKNQKHREILTPNNRYTTPSKARNQCLKETPI 480
 QY 481 KIPVNSTGTDKLMGTGVISPERRCRSVELDLNOAHMEETPKRGAKVFGSLERGLDKVITV 540
 DB 481 KIPVNSTGTDKLMGTGVISPERRCRSVELDLNOAHMEETPKRGAKVFGSLERGLDKVITV 540
 QY 541 LTRSKKSGSARDGPRELKLHYNVTTTRELNVNPOOLNEIMSLPKKHVDVFQKGYTLKCO 600
 DB 541 LTRSKKSGSARDGPRELKLHYNVTTTRELNVNPOOLNEIMSLPKKHVDVFQKGYTLKCO 600
 QY 601 QSDFGKVTMQFELEVQLOKQPDVVGIRRQRLKGDAMVYKRLVEDILSSCKV 651
 DB 601 QSDFGKVTMQFELEVQLOKQPDVVGIRRQRLKGDAMVYKRLVEDILSSCKV 651

RESULT 9

ADN06036
 ID ADN06036 standard; protein; 651 AA.
 XX AC ADN06036;
 XX DT 01-JUL-2004 (first entry)
 XX DE Antipsoriatic protein sequence #1174.
 XX KW antipsoriatic; gene therapy; psoriasis; diagnosis.
 XX OS Homo sapiens.
 XX PN WO2004028479-A2.
 XX PD 08-APR-2004.
 XX PF 25-SEP-2003; 2003WO-US030907.
 XX PR 25-SEP-2002; 2002US-0414006P.
 XX PA (GETH) GENENTECH INC.
 XX PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
 XX WU TD;
 XX WPI; 2004-305105/28.
 XX DR N-PSDB; ADN06035.
 XX PT New PRO nucleic acid or polypeptide, useful for preparing a
 XX PT pharmaceutical composition for diagnosing or treating psoriasis in a
 XX PT mammal.
 XX PS Claim 9; SEQ ID NO 2431; 3069pp; English.
 XX CC The invention relates to novel polynucleotide and polypeptides for
 XX CC treating psoriasis or a sequence having at least 80% identity to the
 XX CC above sequences. The nucleic acid is useful for preparing a composition
 XX CC for diagnosing or treating psoriasis in a mammal. This sequence
 XX CC corresponds to one of the polypeptides of the invention.
 XX Sequence 651 AA;
 SQ

Query Match 100.0%; Score 3447; DB 8; Length 651;
 Best Local Similarity 100.0%; Pred. No. 1.2e-294;
 Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
ADU06466
ID ADU06466 standard; protein; 651 AA.
XX
AC ADU06466;
XX
DT 27-JAN-2005 (first entry)
XX
DE Novel bronchial cancer-associated human protein SeqID690.
XX
KW bronchial cancer; cytostatic; tumour-associated protein;
KW cancer detection; metastasis; tumour; human.
XX
OS Homo sapiens.
XX
PN DE10316701-A1.
XX
PD 04-NOV-2004.
XX
PF 09-APR-2003; 2003DE-01016701.
XX
PR 09-APR-2003; 2003DE-01016701.
XX
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
XX
PI Mennerich D, Bruemendorf T, Heiden E, Hermann K, Kinnemann H;
PI Li X, Roepcke S, Staub E, Hinzmann B, Rosenthal A, Pillareky C;
XX
DR WPI; 2004-786403/78.
DR N-PSDB; ADU05979.
XX
PT New nucleic acid, and derived proteins, useful for diagnosis of bronchial
PT cancer and in screening for therapeutic and diagnostic agents.
XX
PS Claim 2; SEQ ID NO 690; 1381pp; German.
XX
CC This invention relates to a novel isolated nucleic acid associated with
CC bronchial cancer comprising 489 defined sequences given in the
CC specification. The invention may be useful for the production of
CC compounds with a cytostatic activity through the inhibition of expression
CC or activity of tumour-associated proteins. The novel DNA sequences and
CC the proteins/peptides encoded by them are used for detecting bronchial
CC cancer or determining the risk of developing it and to screen for
CC specific binding partners of the DNA or protein sequences, where the
CC binding partners are potentially useful as agents for treating or
CC diagnosing bronchial cancer. The DNA or protein sequences can also be
CC used for prognosis, detection of metastases and for secondary treatment
CC (of tumours that have been stabilised or are no longer detectable).
CC Detecting abnormal expression of the DNA sequences provides early
CC diagnosis of bronchial cancers. The present sequence is that of a protein
CC encoded by a novel bronchial cancer-associated human gene sequence of the
CC invention.
XX
SQ Sequence 651 AA;

Query Match 100.0%; Score 3447; DB 8; Length 651;
Best Local Similarity 100.0%; Pred. No. 1.2e-294;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDYDELLKYELHETIGTGFAKVKLACHILTGEMVAIKIMDKNTLGSDDLPRIKTEIEA 60
DB 1 MKDYDELLKYELHETIGTGFAKVKLACHILTGEMVAIKIMDKNTLGSDDLPRIKTEIEA 60
QY 61 LKNLRHQHICOLYHVLETANKIFWVLEYCPGGELEFDYIISQRLSBEETRVVFRQIVSAV 120
DB 61 LKNLRHQHICOLYHVLETANKIFWVLEYCPGGELEFDYIISQRLSBEETRVVFRQIVSAV 120
QY 121 AYVHSQGYAHRDLKPNLLFDEYHKLKLDLFGLCAPKGNKDYHLQTCGSLAYAAPELI 180
DB 121 AYVHSQGYAHRDLKPNLLFDEYHKLKLDLFGLCAPKGNKDYHLQTCGSLAYAAPELI 180

QY 181 QGKSYLGSEADYVSMGILLIYVLMCGFLPFDDNNVVALYKKIMRGKYDVPKWLSPSSILL 240
DB 181 QGKSYLGSEADYVSMGILLIYVLMCGFLPFDDNNVVALYKKIMRGKYDVPKWLSPSSILL 240
QY 241 QQMLQVDPKKRI SMKNLLNHPIMODYNYVPVWQSKNPFILHDDDCVTEL SVHHRNNROT 300
DB 241 QQMLQVDPKKRI SMKNLLNHPIMODYNYVPVWQSKNPFILHDDDCVTEL SVHHRNNROT 300
QY 301 MEDLISLMOYDHLTATYLLALLAKKARGKPVRLRLSLFSFCQASATPFTDIKNNWSLEDV 360
DB 301 MEDLISLMOYDHLTATYLLALLAKKARGKPVRLRLSLFSFCQASATPFTDIKNNWSLEDV 360
QY 361 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSFTKYWTESNGVESKSLTPALCPTPANKL 420
DB 361 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSFTKYWTESNGVESKSLTPALCPTPANKL 420
QY 421 KKNENYVTPKSAVKNEEYFMFPEKTPVNKNQHKREILTTNRYTTPSKARNOCLKETPI 480
DB 421 KKNENYVTPKSAVKNEEYFMFPEKTPVNKNQHKREILTTNRYTTPSKARNOCLKETPI 480
QY 481 KIPVNSTGDKLMTGVISPERCRSVELDLNQAHEETPKRGAKVFGSLERGLDKVITV 540
DB 481 KIPVNSTGDKLMTGVISPERCRSVELDLNQAHEETPKRGAKVFGSLERGLDKVITV 540
QY 541 LTRSRKGSARDGPRRLKLHYNTTTRLVNPDQLNEIMSILPKGHVDFVQGYTLKCOF 600
DB 541 LTRSRKGSARDGPRRLKLHYNTTTRLVNPDQLNEIMSILPKGHVDFVQGYTLKCOF 600
QY 601 QSDFGKVTMQLFEVLCQKQPDVVGIRQRKLGDAWVYKRLVEDILSSCKV 651
DB 601 QSDFGKVTMQLFEVLCQKQPDVVGIRQRKLGDAWVYKRLVEDILSSCKV 651

RESULT 12
ADX07297
ID ADX07297 standard; protein; 651 AA.
XX
AC ADX07297;
XX
DT 21-APR-2005 (first entry)
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 1862.
XX
KW cytostatic; cyclin-dependent kinase; cdk; biomarker.
OS Homo sapiens.
XX
PN WO2005012875-A2.
PD 10-FEB-2005.
PF 29-JUL-2004; 2004WO-US024424.
PR 29-JUL-2003; 2003US-0490890P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX
DR WPI; 2005-163068/17.
DR N-PSDB; ADX07296.
XX
PT Biomarkers useful for predicting or determining the response of a mammal
PT to a cancer treatment comprising administration of a modulator of cyclin-
PT dependent kinase activity.
XX
PS Claim 5; SEQ ID NO 1862; 141pp; English.
CC This invention describes a novel method of predicting or determining
CC whether a mammal will respond or is responding to an anti-cancer agent
CC that modulates cyclin-dependent kinase (cdk) activity. The method
CC comprises measuring the level of one or more biomarkers selected from
CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID

CC	NO:1246 (Genbank EST W28729) is especially preferred). The method of the invention is utilized in a kit for determining or predicting whether patient would be susceptible or resistant to treatment by an agent modulating cdk activity. The invention also describes a method for utilizing individualized genetic profiles for treating diseases and disorders based on patient's response and molecular level, specialized microarrays comprising the biomarkers described, antibodies directed against the biomarkers and a cell culture model to identify biomarkers. The cdk modulator is preferably N-5-[(5-(1,1-Dimethylethyl)-2-oxazolyl)methyl]thiol-2-thiazolyl-4-piperidine carboxamide, 0.5-l-tartaric acid salt. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. This sequence represents a biomarker used in the method of the invention.	XX	Human maternal embryonic leucine zipper kinase, MELK.
CC		DE	
CC		XX	Maternal embryonic leucine zipper kinase; enzyme; drug screening;
CC		KW	angiogenesis disorder; antiangiogenic; cardiovascular disease; apoptosis;
CC		KW	cancer; cycostatic; neoplasm; diagnosis; gene therapy.
CC		XX	Homo sapiens.
CC		XX	Key Location/Qualifiers
CC		FT	Domain 11..263
CC		FT	/label = Kinase_domain
CC		FT	Domain 602..651
CC		FT	/label = Kinase_associated_domain_1
CC		XX	WO2005016279-A2.
CC		XX	
CC		PD	24-FEB-2005.
CC		XX	
CC		PF	12-AUG-2004; 2004WO-US026231.
CC		XX	
CC		PR	14-AUG-2003; 2003US-0495193P.
CC		XX	
CC		PA	(EXEL-) EXELIXIS INC.
CC		XX	
CC		PI	Kadyk L, Francis GR, Heuer TS, Lickteig K;
CC		XX	
CC		DR	WPI; 2005-173218/18.
CC		DR	N-PSDB; ADW93565, ADW93566, ADW93569.
CC		XX	
CC		PT	Identifying candidate RAC pathway modulating agents useful for diagnosing or treating e.g. cancer, comprises screening for agents that modulate the activity of Maternal Embryonic Leucine Zipper Kinase (MELK).
CC		PT	
CC		XX	Example 1; SEQ ID NO 6; 52pp; English.
CC		PS	
CC		XX	The invention relates to identifying a candidate RAC pathway modulating agent comprising screening for agents that modulate the activity of Maternal Embryonic Leucine Zipper Kinase (MELK). Also included are modulating a RAC pathway of a cell or in a mammalian cell and diagnosing a disease in a patient. In identifying a candidate RAC pathway-modulating agent, the assay system comprises cultured cells that express the MELK polypeptide. The cultured cells additionally have defective RAC function. The methods are useful for diagnosing or treating cancer or for identifying modulators of RAC pathway, which may be utilized as therapeutic targets for disorders associated with defective RAC function, such as cancer, angiogenic disorder and apoptotic disorders. The present sequence represents human MELK.
CC		XX	
CC		SQ	Sequence 651 AA;
CC			Query Match 100.0%; Score 3447; DB 9; Length 651;
CC			Best Local Similarity 100.0%; Pred. No. 1.2e-294;
CC			Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MKDYDELLKYYELHETIGTGGFAKVKLACHILTGEMVAIKIMDKNTLGSDDLPRIKTEIEA 60	Qy	1 MKDYDELLKYYELHETIGTGGFAKVKLACHILTGEMVAIKIMDKNTLGSDDLPRIKTEIEA 60
Db	1 MKDYDELLKYYELHETIGTGGFAKVKLACHILTGEMVAIKIMDKNTLGSDDLPRIKTEIEA 60	Db	1 MKDYDELLKYYELHETIGTGGFAKVKLACHILTGEMVAIKIMDKNTLGSDDLPRIKTEIEA 60
Qy	61 LKNLRHQHICQLYHVLETANKIPMWLEYCPGGELFDYIISQDRLSEETRVVFRQIVSAV 120	Qy	61 LKNLRHQHICQLYHVLETANKIPMWLEYCPGGELFDYIISQDRLSEETRVVFRQIVSAV 120
Db	61 LKNLRHQHICQLYHVLETANKIPMWLEYCPGGELFDYIISQDRLSEETRVVFRQIVSAV 120	Db	61 LKNLRHQHICQLYHVLETANKIPMWLEYCPGGELFDYIISQDRLSEETRVVFRQIVSAV 120
Qy	121 AYVHSGQYAHARDLKPENLLFDEYHKLLIDFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180	Qy	121 AYVHSGQYAHARDLKPENLLFDEYHKLLIDFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180
Db	121 AYVHSGQYAHARDLKPENLLFDEYHKLLIDFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180	Db	121 AYVHSGQYAHARDLKPENLLFDEYHKLLIDFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180
Qy	181 QGKSYLGSEADVMSGILLVLMCGFLPFDDNNVMAKYKIMRGKYDVPKWLSPSSILL 240	Qy	181 QGKSYLGSEADVMSGILLVLMCGFLPFDDNNVMAKYKIMRGKYDVPKWLSPSSILL 240
Db	181 QGKSYLGSEADVMSGILLVLMCGFLPFDDNNVMAKYKIMRGKYDVPKWLSPSSILL 240	Db	181 QGKSYLGSEADVMSGILLVLMCGFLPFDDNNVMAKYKIMRGKYDVPKWLSPSSILL 240
Qy	241 QQMLQVDPKCRISMKNLLNHPMTMODYNTYVMEQSKNPETHLDDDCVTELSVHHRNROT 300	Qy	241 QQMLQVDPKCRISMKNLLNHPMTMODYNTYVMEQSKNPETHLDDDCVTELSVHHRNROT 300
Db	241 QQMLQVDPKCRISMKNLLNHPMTMODYNTYVMEQSKNPETHLDDDCVTELSVHHRNROT 300	Db	241 QQMLQVDPKCRISMKNLLNHPMTMODYNTYVMEQSKNPETHLDDDCVTELSVHHRNROT 300
Qy	301 MEDLISLMQVHDLTATYVLLLAKKARGKPVRLRLSPFCQASATPFTDIKSNNWSLEDV 360	Qy	301 MEDLISLMQVHDLTATYVLLLAKKARGKPVRLRLSPFCQASATPFTDIKSNNWSLEDV 360
Db	301 MEDLISLMQVHDLTATYVLLLAKKARGKPVRLRLSPFCQASATPFTDIKSNNWSLEDV 360	Db	301 MEDLISLMQVHDLTATYVLLLAKKARGKPVRLRLSPFCQASATPFTDIKSNNWSLEDV 360
Qy	361 TASDKNVAAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420	Qy	361 TASDKNVAAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
Db	361 TASDKNVAAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420	Db	361 TASDKNVAAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
Qy	421 XNKENVYTPKSAVKNEBEYFMFPBPPTPVNKNQHKREILTPPNRYTTPSKARNQCLKETPI 480	Qy	421 XNKENVYTPKSAVKNEBEYFMFPBPPTPVNKNQHKREILTPPNRYTTPSKARNQCLKETPI 480
Db	421 XNKENVYTPKSAVKNEBEYFMFPBPPTPVNKNQHKREILTPPNRYTTPSKARNQCLKETPI 480	Db	421 XNKENVYTPKSAVKNEBEYFMFPBPPTPVNKNQHKREILTPPNRYTTPSKARNQCLKETPI 480
Qy	481 KIPVNSTGTDKLMGTVISPPRRCSRVELDLNQAHMEETPRKGAKVFGSLERGLDKVITV 540	Qy	481 KIPVNSTGTDKLMGTVISPPRRCSRVELDLNQAHMEETPRKGAKVFGSLERGLDKVITV 540
Db	481 KIPVNSTGTDKLMGTVISPPRRCSRVELDLNQAHMEETPRKGAKVFGSLERGLDKVITV 540	Db	481 KIPVNSTGTDKLMGTVISPPRRCSRVELDLNQAHMEETPRKGAKVFGSLERGLDKVITV 540
Qy	541 LTRSKRGSGARDGPRRLKHLHYNTTTLVNPDLNMEIMSLPKGHVDVFOKGTYTLKQOT 600	Qy	541 LTRSKRGSGARDGPRRLKHLHYNTTTLVNPDLNMEIMSLPKGHVDVFOKGTYTLKQOT 600
Db	541 LTRSKRGSGARDGPRRLKHLHYNTTTLVNPDLNMEIMSLPKGHVDVFOKGTYTLKQOT 600	Db	541 LTRSKRGSGARDGPRRLKHLHYNTTTLVNPDLNMEIMSLPKGHVDVFOKGTYTLKQOT 600
Qy	601 QSDFGKVTMQFELEVCOQLKPDVVVGIRRRQLKGDWVYKRLVEDILSSCKV 651	Qy	601 QSDFGKVTMQFELEVCOQLKPDVVVGIRRRQLKGDWVYKRLVEDILSSCKV 651
Db	601 QSDFGKVTMQFELEVCOQLKPDVVVGIRRRQLKGDWVYKRLVEDILSSCKV 651	Db	601 QSDFGKVTMQFELEVCOQLKPDVVVGIRRRQLKGDWVYKRLVEDILSSCKV 651
CC	RESULT 13	CC	
CC	ADW93570	CC	
ID	ADW93570 standard; protein; 651 AA.	ID	
XX		XX	
AC	ADW93570;	AC	
XX		XX	
DT	05-MAY-2005 (first entry)	DT	

Db 241 QQMLQVDPKKRISMKNLNHPWIMQDYNYPVEWQSKNPFILHDDDCVTELSVHHRNRQT 300
 QY 301 MEDLISLWQYDHLTATYLLALLAKARGKPVRLRLSSFCQASATPFTDIKSNWNSLEDV 360
 Db 301 MEDLISLWQYDHLTATYLLALLAKARGKPVRLRLSSFCQASATPFTDIKSNWNSLEDV 360
 QY 361 TASDKNYVAGLIDYDCCEDDLSTGAATPRTSQFTKYWTESNGVSKSLTPALCRTPANKL 420
 Db 361 TASDKNYVAGLIDYDCCEDDLSTGAATPRTSQFTKYWTESNGVSKSLTPALCRTPANKL 420
 QY 421 KKNENVYTPKSAVKNEEYFMFPBKTPVNKNQHKREILTPNRYTTPSKARNOCLEKTP 480
 Db 421 KKNENVYTPKSAVKNEEYFMFPBKTPVNKNQHKREILTPNRYTTPSKARNOCLEKTP 480
 QY 481 KIPVNSTGDKLMTGVISPERCRSVELDLNQAHMEETPKRGAKVFGSLERGLDKVITV 540
 Db 481 KIPVNSTGDKLMTGVISPERCRSVELDLNQAHMEETPKRGAKVFGSLERGLDKVITV 540
 QY 541 LTRSKRKSARDGPRRLKLYNVTTRLVNPDQLLNEIMSILPKKHVDVFQKGYTLKCO 600
 Db 541 LTRSKRKSARDGPRRLKLYNVTTRLVNPDQLLNEIMSILPKKHVDVFQKGYTLKCO 600
 QY 601 QSDFGKVTMQFELEVQCOLQKPDVVGIRRORLKGDAWYKRLVEDILSSCKV 651
 Db 601 QSDFGKVTMQFELEVQCOLQKPDVVGIRRORLKGDAWYKRLVEDILSSCKV 651

RESULT 14

ADV15428

ID ADY15428 standard; protein; 651 AA.

XX AC ADY15428;

XX DT 05-MAY-2005 (first entry)

XX DE PRO polypeptide SEQ ID NO 1234.

XX KW Antinflammatory; Immune disorder; Dermatological; Immunosuppressive;

XX KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;

XX KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;

XX KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;

XX KW Antiallergic; ds; gene; diagnosis.

XX OS Homo sapiens.

XX PN WO2005016962-A2.

XX PD 24-FEB-2005.

XX PF 11-AUG-2004; 2004WO-US026249.

XX PR 11-AUG-2003; 2003US-0493546P.

XX PA (GETH) GENENTECH INC.

XX PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX DR WPI; 2005-182330/19.

XX FT New nucleic acid encoding PRO polypeptide, useful for diagnosing and

XX FT treating an immune related disorder, e.g. systemic lupus erythematosus,

XX FT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

XX PS Claim 8; SEQ ID NO 1234; 158pp; English.

XX CC The invention relates to an isolated nucleic acid encoding a PRO

XX CC polypeptide. The polypeptide, agonist or an antagonist, antibody,

XX CC composition, and method are useful for diagnosing and treating an immune

XX CC related disorder, e.g. systemic lupus erythematosus, rheumatoid

XX CC arthritis. The present sequence represents a DNA encoding a PRO

XX CC polypeptide.

XX SQ Sequence 651 AA;

Query Match 100.0%; Score 3447; DB 9; Length 651;
 Best Local Similarity 100.0%; Pred. No. 1.2e-294;
 Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDYDELLAKYVYELHETIGTGGAFAKVKLACHILTGEMVAIKIMDKNTLGSGLPRIKTEIEA 60
 Db 1 MKDYDELLAKYVYELHETIGTGGAFAKVKLACHILTGEMVAIKIMDKNTLGSGLPRIKTEIEA 60
 QY 61 LKNLRHQHICQLYHYVLELTANKIFMWLEYCPGGELFDYIIISQRLSEETRVVFRQIVSAV 120
 Db 61 LKNLRHQHICQLYHYVLELTANKIFMWLEYCPGGELFDYIIISQRLSEETRVVFRQIVSAV 120
 QY 121 AYVHSGYAHARDLKPENLLFDEYHKLKLDLFGLCAPKGNKDYHLQTCGSLAYAAPELI 180
 Db 121 AYVHSGYAHARDLKPENLLFDEYHKLKLDLFGLCAPKGNKDYHLQTCGSLAYAAPELI 180
 QY 181 QKSYLGSADYVWSGILLVLMCGFLPDDDNVVALYKKIMRGKYDVPKWLSPSSILL 240
 Db 181 QKSYLGSADYVWSGILLVLMCGFLPDDDNVVALYKKIMRGKYDVPKWLSPSSILL 240
 QY 241 QQMLQVDPKKRISMKNLNHPWIMQDYNYPVEWQSKNPFILHDDDCVTELSVHHRNRQT 300
 Db 241 QQMLQVDPKKRISMKNLNHPWIMQDYNYPVEWQSKNPFILHDDDCVTELSVHHRNRQT 300
 QY 301 MEDLISLWQYDHLTATYLLALLAKARGKPVRLRLSSFCQASATPFTDIKSNWNSLEDV 360
 Db 301 MEDLISLWQYDHLTATYLLALLAKARGKPVRLRLSSFCQASATPFTDIKSNWNSLEDV 360
 QY 361 TASDKNYVAGLIDYDCCEDDLSTGAATPRTSQFTKYWTESNGVSKSLTPALCRTPANKL 420
 Db 361 TASDKNYVAGLIDYDCCEDDLSTGAATPRTSQFTKYWTESNGVSKSLTPALCRTPANKL 420
 QY 421 KKNENVYTPKSAVKNEEYFMFPBKTPVNKNQHKREILTPNRYTTPSKARNOCLEKTP 480
 Db 421 KKNENVYTPKSAVKNEEYFMFPBKTPVNKNQHKREILTPNRYTTPSKARNOCLEKTP 480
 QY 481 KIPVNSTGDKLMTGVISPERCRSVELDLNQAHMEETPKRGAKVFGSLERGLDKVITV 540
 Db 481 KIPVNSTGDKLMTGVISPERCRSVELDLNQAHMEETPKRGAKVFGSLERGLDKVITV 540
 QY 541 LTRSKRKSARDGPRRLKLYNVTTRLVNPDQLLNEIMSILPKKHVDVFQKGYTLKCO 600
 Db 541 LTRSKRKSARDGPRRLKLYNVTTRLVNPDQLLNEIMSILPKKHVDVFQKGYTLKCO 600
 QY 601 QSDFGKVTMQFELEVQCOLQKPDVVGIRRORLKGDAWYKRLVEDILSSCKV 651
 Db 601 QSDFGKVTMQFELEVQCOLQKPDVVGIRRORLKGDAWYKRLVEDILSSCKV 651

RESULT 15

ADY20530

ID ADY20530 standard; protein; 651 AA.

XX AC ADY20530;

XX DT 05-MAY-2005 (first entry)

XX DE PRO polypeptide SEQ ID NO 6336.

XX KW Antinflammatory; Immune disorder; Dermatological; Immunosuppressive;

XX KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;

XX KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;

XX KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;

XX KW Antiallergic; diagnosis.

XX OS Homo sapiens.

XX PN WO2005016962-A2.

XX PD 24-FEB-2005.

XX PF 11-AUG-2004; 2004WO-US026249.

Job time : 206 secs

```
XX 11-AUG-2003; 2003US-0493546P.
XX (GETH ) GENENTECH INC.
XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
XX WPI; 2005-182330/19.
XX
XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
XX treating an immune related disorder, e.g. systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX
XX Claim 8; SEQ ID NO 6336; 158pp; English.
XX
XX The invention relates to an isolated nucleic acid encoding a PRO
XX polypeptide. The polypeptide, agonist or an antagonist, antibody,
XX composition, and method are useful for diagnosing and treating an immune
XX related disorder, e.g. systemic lupus erythematosus, rheumatoid
XX arthritis. The present sequence represents a PRO polypeptide.
XX
XX Sequence 651 AA;
XX
Query Match      100.0%; Score 3447; DB 9; Length 651;
Best Local Similarity 100.0%; Pred. No. 1.2e-294;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKDYDELLKYYEHEHTGTGGFAKVKLACHILTGEMVAIKIMDKNTLGSGLPRIKTEIEA 60
DB 1 MKDYDELLKYYEHEHTGTGGFAKVKLACHILTGEMVAIKIMDKNTLGSGLPRIKTEIEA 60
QY 61 LKNLRHQHICQLVHLETKANKIPWLEYCPGGELFDYIISQDRLSEETRVVFRQIVSAV 120
DB 61 LKNLRHQHICQLVHLETKANKIPWLEYCPGGELFDYIISQDRLSEETRVVFRQIVSAV 120
QY 121 AYVHSQGYAHRDLKPNLLPDEYHKLIDFGICAKPGKNKYHLQTCGSLAYAAPELI 180
DB 121 AYVHSQGYAHRDLKPNLLPDEYHKLIDFGICAKPGKNKYHLQTCGSLAYAAPELI 180
QY 181 QGKSYLGSEADVMSGILLVYLMCGELPDDDDNMALYKKIMRGKYDVPKWLSPSSILL 240
DB 181 QGKSYLGSEADVMSGILLVYLMCGELPDDDDNMALYKKIMRGKYDVPKWLSPSSILL 240
QY 241 QQMLQVDPKKRI SMKNLLNHPIMQDYNYPVEWQSKNPF IHLDDDCVTLSVHRRNRQT 300
DB 241 QQMLQVDPKKRI SMKNLLNHPIMQDYNYPVEWQSKNPF IHLDDDCVTLSVHRRNRQT 300
QY 301 MEDLISLWQYDHLTATYVLLLLAKKARGKPVRLRLSSPCQASATPFTDIKSNNWSLEDV 360
DB 301 MEDLISLWQYDHLTATYVLLLLAKKARGKPVRLRLSSPCQASATPFTDIKSNNWSLEDV 360
QY 361 TASDKNNVAGLIDYDCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
DB 361 TASDKNNVAGLIDYDCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
QY 421 KKNENVYTPKSAVKNEEYFMFPKPTPVNKNQHKREILITPNRYTTPSKARNQCLKETPI 480
DB 421 KKNENVYTPKSAVKNEEYFMFPKPTPVNKNQHKREILITPNRYTTPSKARNQCLKETPI 480
QY 481 KIPVNSTGTDKLMTGVISPERRCRSVELDLNQAHMEETPKRGAKVFGSLERGLDKVITV 540
DB 481 KIPVNSTGTDKLMTGVISPERRCRSVELDLNQAHMEETPKRGAKVFGSLERGLDKVITV 540
QY 541 LITSKRKGSARDGPRRLKLNHYNTTTLVNPDDLLNEIMSLPKKHVDVFOKGYTLKCO 600
DB 541 LITSKRKGSARDGPRRLKLNHYNTTTLVNPDDLLNEIMSLPKKHVDVFOKGYTLKCO 600
QY 601 QSDFGKVTMQFELEVCOLOKPDVVGIRRRORLKGDAWYKRLVEDILSSCKV 651
DB 601 QSDFGKVTMQFELEVCOLOKPDVVGIRRRORLKGDAWYKRLVEDILSSCKV 651
```

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: November 21, 2006, 14:08:31 ; Search time 44 Seconds
(without alignments)
1423.571 Million cell updates/sec

Title: US-10-656-598-2

Perfect score: 3447

Sequence: 1 MKDYDELLKYYELHETIGT.....KGDWVYKRLVEDILSSCKV 651

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2107	61.1	651	2 S52244	p69Eg3 protein - A
2	1156	33.5	726	2 T33998	hypothetical prote
3	789.5	22.9	713	2 S27966	probable serine/th
4	762.5	22.1	745	2 G01025	serine/threonine p
5	712.5	20.7	774	2 I48609	probable serine/th
6	690.5	20.0	1192	2 T18611	probable serine/th
7	690.5	20.0	1246	2 G89287	protein H39E23.1
8	648	18.8	513	1 S60303	serine/threonine-s
9	647	18.8	552	1 S51025	[hydroxymethyl]glut
10	644	18.7	552	1 A53621	[hydroxymethyl]glut
11	641.5	18.6	504	2 T10449	probable serine/th
12	640.5	18.6	504	2 T07415	probable serine/th
13	637	18.5	512	1 JCI446	serine/threonine-s
14	637	18.5	513	1 S60304	serine/threonine-s
15	636	18.5	602	2 S72513	POG2 protein - yea
16	635	18.4	633	1 A26030	serine/threonine-s
17	630	18.3	512	2 T52633	serine/threonine-s
18	627	18.2	480	2 A86427	probable serine/th
19	627	18.2	562	2 T29858	hypothetical prote
20	625	18.1	472	2 B90100	SNF-related kinase
21	624.5	18.1	511	1 A56009	serine/threonine-s
22	624	18.1	891	2 T40503	protein kinase kin
23	623	18.1	891	2 A38903	protein kinase 1 -
24	622	18.0	441	2 JCY500	qik protein - chic
25	618.5	17.9	798	2 S59941	serine/threonine-s
26	615.5	17.9	473	1 S59941	serine/threonine-s
27	611	17.7	502	1 A41361	probable serine/th
28	610.5	17.7	512	2 T07788	hypothetical prote
29	608.5	17.7	887	2 T20941	

30	608	17.6	510	2 T04145	serine/threonine p
31	606.5	17.6	440	2 T14736	probable serine/th
32	606.5	17.6	440	2 T14735	probable serine/th
33	605.5	17.6	445	2 T50802	serine/threonine p
34	605.5	17.6	481	2 I49072	protein kinase - m
35	605	17.6	1398	2 T13741	hypothetical prote
36	601.5	17.4	576	2 T41587	probable carbon ca
37	595	17.3	445	2 T09903	serine/threonine-s
38	593	17.2	435	2 E84707	probable protein k
39	593	17.2	502	2 T02306	probable protein k
40	592	17.2	489	2 T04862	probable serine/th
41	592	17.2	746	2 S62365	SNF1-related prote
42	588.5	17.1	622	1 S44859	serine/threonine-s
43	587.5	17.0	442	2 T48203	hypothetical prote
44	579	16.8	426	2 C71408	probable protein k
45	578.5	16.8	453	2 G86141	protein T25K16.13

ALIGNMENTS

RESULT 1

S52244

p69Eg3 protein - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004

C:Accession: S52244

R:Roghi, C.; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.

A:Description: Eg3, selected by differential screening encodes a new Xenopus protein kin

A:Reference number: S52243

A:Accession: S52244

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-651 <ROG>

A:Cross-references: UNIPROT:Q91821; UNIPARC:UPI000017A463; EMBL:Z17205; NID:g609283; PID:

C:Keywords: ATP

F:11-265/Domain: protein kinase homology <KIN>

F:19-27/Region: protein kinase ATP-binding motif

Query Match 61.1%; Score 2107; DB 2; Length 651;

Best Local Similarity 62.0%; Pred. No. 2.6e-85;

Matches 410; Conservative 87; Mismatches 138; Indels 26; Gaps 8;

QY	3	DYDELLKYYELHETIGTGGFAKVKLACHILTEGVAIKIMDKNTLGSDDLPRKTEIALK	62
DB	5	DYDELLKYYELHETIGTGGFAKVKLASHLITGEKVAIKIMDKESLGGDLPRVKTEIDAMK	64
QY	63	NURHQHICOLYHVLETANKIFMWLEYCPGGELFDYIIISQDRLSEBETRVVFRQIVSAVAY	122
DB	65	NLSHQHVCRLYHVIETPKKIFMWLEYCPGGELFDYIIANDRLTEBEARVFFRQIVSAVAY	124
QY	123	VHSQGVYHRDLAKPENLLPDEYHKLIDPGLCAKPKGNKDYHLOTCCGSLAAAPLLOQ	182
DB	125	IHSQGVYHRDLAKPENLLPDEYHKLIDPGLCAKPKGNKDYHLOTCCGSLAAAPLLOQ	184
QY	183	KSYLSEADVWSMGILLVYLMCGFLPFDDNNVMALYKKIMRGKYDVPKWLSPSSILLLOQ	242
DB	185	KAYIGSEADVWSMGILLVYLMCGFLPFDDNNVMALYKKIMRGKYDVPKWLSPSSILLLOQ	244
QY	243	MLQVDPKGRKISMKNLNHPWIMQDYNYPVWQSKNPFHLDDDCVTETLSVHHRNRQWTE	302
DB	245	MMQVDPKGRKIRITVKHLNHPWIMHGYSCPVWQSKNPFHLDDDCVTETLSVFKYSTSTT	304
QY	303	DLISLWQVDHLTATYLLALLAKKARGKPVRLRLSSFCGQASATPFTDICKNNWSLDDVTA	362
DB	305	RLISEWSYDHIITASYLLHLLSKKSHKAVLK-HPLAVGQAVTSFKELAPKSLDFEEN	363
QY	363	SDKNVTAVGLIDY---DWCEDDLSTGAATPRT-SQFTKKWTSNGVSKSLTLPALCRTPAN	418
DB	364	GBIAYVFGSMDFSEELFSEDTYSSFEHTPKYVKGRLFNVSVDSPATPVFNAMLGT	423
QY	419	KLNNKENVYTPKSAVK-----NEEYFMPEPPTKPVNKNQHKREILTTNRYTTPSKARNQ	473

Db 404 DHAGPQIPVAVPKRSQSTADSDLKEDGISRSKST-----GSAVGGKGIAP 451
QY 411 A--LCRTPAKGLK-----NKENVYT-----PKSAVKN-EE 437
Db 452 ASPMLGNASNPKNKADIPERKKSSTVPSSNTASGGMTRRTYVCSERTTDDRHSVIQNGKE 511
QY 438 YMFPEPKTPVNQKHREILTT--PNRYTTPSKARNQC-----LKETPIKIPVNSTGTDKLM 493
Db 512 NSTIPQRTPV-ASTHSISAAATPDR-----IRFP-----RGTSASRFTFG 551
QY 498 SP-ERRC-----RSVELDLNQAHEETPKRKGAQVGSLEGLDKVITVLTFS----- 544
Db 552 QPRERTATYNGPPASPSPLSHEATPLSQTSSRGSTTLF-----SKTYSKLTSSRNWSA 604
QY 545 KRKGSARDG-PRRLKLHLYNVTTTTLNPPDQLNEIMSILPKKHVDVQK-GYTLKQQTOS 602
Db 605 KQDENKEAKPRSLRFTWSMKTSSMDPGDMREIRKVLNANCDVEQREFFLFCVHGD 664
QY 603 DFGKVTMQFELEVQLOKQPDVVGIRQRORLKGDAWYKRLVEDILSSCKV 651
Db 665 GHAENLVOMEMEVCKLPRLSLNGVRFKRTISGTSIAPKNTASKIANELKL 713
RESULT 4
G01025
serine/threonine protein kinase - human
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Oct-2004
C:Accession: G01025
R:Navarro, E.
submitted to the EMBL Data Library, April 1996
A:Reference number: H00564
A:Accession: G01025
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-745 <NAV>
A:Cross-references: UNIPROT:Q15524; UNIPROT:Q96HB3; UNIPARC:UPI000017A42B; EMBL:X97630;
F:18-271/Domain: protein kinase homology <KIN>
Query Match 22.1%; Score 762.5; DB 2; Length 745;
Best Local Similarity 29.6%; Pred. No. 1.5e-26;
Matches 220; Conservative 136; Mismatches 267; Indels 121; Gaps 27;
QY 11 YELHETIGTGPAKVKLACHILITGEMVAIKIMDKNTL-GSDLPRIKTEIALKNLRHOHI 69
Db 20 YLLAKTIGKGNPAKVKLARHILITGEVAVKIDKTLQNSSSLQKLFREVRIMKVLNHPNI 79
QY 70 COLYHVLTEANKIFWLEVCYPCGGELFDYIIISODRLSEETRVVFRQIVSAVAYVHSQGYA 129
Db 80 VKLFEVIEETKTLVLMVEYASGGEVDFYLVAHGRMKKEARAKFRQIVSAVQYCHQKFTV 139
QY 130 HRDLKPNLLPDEYHKLIIDFGLCAK-PKGNKDYHLOTCCGSLAYAAPELLQKSYLGS 188
Db 140 HRDLKAENLLDADNMNIKIADFGFSNEFTFGNK---LDTFCGSPPYAAPELFGQKKYDGP 196
QY 189 EADVNSMGLLYLVLMCGFLPFDDNNVMALYKIMRGKYDVPKWLSPSILLQOQLVDP 248
Db 197 EVDVNSGLVILTYLVSGSLPFGQNLKELRERVLRGKTRIPFYMSTDCENLLKKFLINP 256
QY 249 KGRISMKNLLNHPWIMQDYNYPVWQSQKNPFTH-----LDDCCVTSLSHHNRNQTMEEL 304
Db 257 SKRGTLQIMQDRW---NVGHEDDELPYVEPLPDYKPRTELWMSMGYTRBEEIQDS 312
QY 305 ISLWQYDHLTATYILLAKKA--RGKPVRLR-----LSSPSC-----QOASATP-- 346
Db 313 LVQRYNEVMATYLLGLYKSSLEGGDTITLPRPSADLTNSSAQPFSHKVQSVSANPKQ 372
QY 347 --FTD-----IKSNWSLEDVTASDKNVVAGLIDYDWCEDDLSTCAATPRTSQTKYWT 398
Db 373 RRFSDQAGPAITPSNSYKTSQNNNAENKRP-----EEDRESGRKASSTAKVPA--S 422
QY 399 ESNGVESKSLTP-----ALCRTLPAKLNK-----ENVYTPKSAVKN-EEYFMFPEPK----- 445

Db 423 PLPGLERKKTTPPTPTNSVLSTSTRSRNSPLLRASLQASIQNGKOSLTPFGSASTA 482
QY 446 -----TPVNKQKHREILTT--PNRYTTPSKARNQC-----LKETPIKIPVNSTGTDKLM 493
Db 483 SASAGVSAARPRQHQKSMGSHVHPNKAAGLPFTESNCEVPRSTAPQRPVPAVSPSAHNIS 542
QY 494 TQVISPGR-----RCRSVELDLNQAHEETPK-----RKGA--KVP 527
Db 543 SSGGAPDRTNFPRGVSSRSRSTFHAGQLRQVR-DQONLPYGVTPASPSPSGHSGQHRGASGSIF 601
QY 528 GS-----LERGL-----DKVITVLT-----RKRKGSARDG-PRRLKLHLYNVTTTTL 568
Db 602 SKFTSKFVRNNEPESKDRVETLPHVVGSGNDKEKEEFREAKPRSLRFTWSMKTSS 661
QY 569 VNPFDOLLNEIMSILPKKHVDV-FVKGYTLKQQTOSDFGKVTMQFELEVQLOKQPDVVGIR 627
Db 662 MEPNEMREIRKVLNANCDVEQREFFLFCVHGD 664
QY 628 RQRLKGDWYKRLVEDILSSCKV 651
Db 722 FKRTISGTSMAFKNTASKIANELKL 745
RESULT 5
I48609
probable serine/threonine-specific protein kinase (EC 2.7.1.-) kem - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C:Accession: I48609; S31333
R:Ingilis, J.D.; Lee, M.; Hill, R.E.
Mamm. Genome 4, 401-403, 1993
A:Title: Emk, a protein kinase with homologs in yeast maps to mouse chromosome 19.
A:Reference number: I48609; MUID:93364122; PMID:8358177
A:Accession: I48609
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-774 <ING1>
A:Cross-references: UNIPROT:Q05512; UNIPARC:UPI00000275D5; EMBL:X70764; NID:g57919; PIDN:
R:Ingilis, J.D.; Lee, M.; Hill, R.E.
submitted to the EMBL Data Library, January 1993
A:Description: A novel protein kinase with homologues in yeast maps to mouse chromosome 19
A:Reference number: S31333
A:Accession: S31333
A:Molecule type: mRNA
A:Residues: 1-698, 'K', 700-702, 'GRGLPTAAKASCTGTCYCAGMAHQATRT', 731-774 <ING2>
A:Cross-references: UNIPARC:UPI000017A424; EMBL:X70764
C:Genetics:
A:Gene: emk
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:51-304/Domain: protein kinase homology <KIN>
F:59-67/Region: protein kinase ATP-binding motif
Query Match 20.7%; Score 712.5; DB 2; Length 774;
Best Local Similarity 28.6%; Pred. No. 2.4e-24;
Matches 210; Conservative 138; Mismatches 282; Indels 103; Gaps 25;
QY 11 YELHETIGTGPAKVKLACHILITGEMVAIKIMDKNTL-GSDLPRIKTEIALKNLRHOHI 69
Db 53 YRLKTIQKGNPAKVKLARHILITGEVAVKIDKTLQNSSSLQKLFREVRIMKVLNHPNI 112
QY 70 COLYHVLTEANKIFWLEVCYPCGGELFDYIIISODRLSEETRVVFRQIVSAVAYVHSQGYA 129
Db 113 VKLFEVIEETKTLVLMVEYASGGEVDFYLVAHGRMKKEARAKFRQIVLHVQYCHQKFTV 172
QY 130 HRDLKPNLLPDEYHKLIIDFGLCAK-PKGNKDYHLOTCCGSLAYAAPELLQKSYLGS 188
Db 173 HRDLKAENLLDADNMNIKIADFGFSNEFTFGNK---LDTFCGSPPYAAPELFGQKKYDGP 229
QY 189 EADVNSMGLLYLVLMCGFLPFDDNNVMALYKIMRGKYDVPKWLSPSILLQOQLVDP 248
Db 230 EVDVNSGLVILTYLVSGSLPFGQNLKELRERVLRGKTRIPFYMSTDCENLLKKFLINP 289

A:Map position: 5

Query Match	20.0%;	Score 690.5;	DB 2;	Length 1246;
Best Local Similarity	31.7%;	Prod No 3	58-23.	

[illegible]

RESULT 8

S60303
serine/threonine-specific protein kinase (EC 2.7.1.-) BKIN12 (version 1) - barley
C:Species: Hordeum vulgare (barley)
C:Date: 20-Jul-1996 #sequence_revision 27-Feb-1997 #text_change 05-Oct-2004
C:Accession: S60303; S24578
R:Halford, N.G.; Vicente-Carbaljosa, J.; Sabelli, P.A.; Shewry, P.R.; Hannappel, U.; Kreis
Plant J. 2, 791-797, 1992
A:Title: Molecular analyses of a barley multigene family homologous to the yeast protein
A:Reference number: S60303; MUID:93258420; PMID:1302632
A:Accession: S60303
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-513 <HAL>
A:Cross-references: UNIPROT:Q40029; UNIPARC:UP1000000A154A; EMBL:X65606; NID:g18931; PIDN
C:Genetics:
A:Introns: 62/1; 126/3; 187/3; 231/3; 293/3; 323/3; 351/3; 398/3; 476/3
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C:Superfamily: SNF1-related protein kinase; protein kinase homology
C:Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F:15-272/Domain: protein kinase homology <KIN>
F:23-31/Region: protein kinase ATP-binding motif
F:46,65,143,145/Active site: Lys, Glu, Asp, Lys #status predicted
F:148,152/Binding site: magnesium (Asn, Asp)#status predicted

[illegible]

RESULT 9

[illegible]

Query Match 18.8%; Score 647; DB 1; Length 552;
Best Local Similarity 43.3%; Pred. No. 1.2e-21;
Matches 139; Conservative 51; Mismatches 115; Indels 16; Gaps 6;

QY 10 YYELHETIGTGGAFAKVLACHILTGEMVAIKMDKNTLGS--DLPRKTEIEALKNLRHQ 67
DB 15 HYLVDGLTGVGTGKVKIGESHQTHGKVAVKILNRQKIRSLDVVGKIKREIQNLKLFRRP 74

QY 68 HICQLYHVLTEANKIFMWLEFCPGGELFDYIIISQDLSEETRVPRQIVSAVAVHSQG 127
DB 75 HIILKLVQVISTPTDFWMVEYSGGELFDYICKGRVEVEARRLFFQQLSAVDYCHRRM 134

QY 128 YAHRLDKPENLLDEYHKLKLDIFGLCAKPKGNKDYHLQTCGSLAYAAPELIQGSYLG 187
DB 135 VVRDLKPEVLLDAHNAKIADFGLSNMMSDGE--FLRTSCGSPNYAAPEVISGRLYAG 192

QY 188 SEADVWSMGLLYVLMCGFLPDDNNMVALYKKIMRGKYDVPKWLSPSSILLLOQMLOYD 247
DB 193 PEVDIWSGCVILYALLCGTLPDDHVPFLFKIRGGVFYIPEYLNRSVATLLMHMLQYD 252

QY 248 PKKRISMKNLNHPWIMQD---YNYPVWQSKNPFTH---LDDDCVTELSVHHR-NNRQT 300
DB 253 PLKRATIKDIRHEWFKQDLPVSLFP-----EDPSYDANVIDEAVKEVCEKPECTESEV 307

QY 301 MEDLISLMQYDHLTATYLLLL 321
DB 308 MNSLYSGDPQDLAVAYHLII 328

RESULT 10
A53621
[hydroxymethylglutaryl-CoA reductase (NADPH2)] kinase (EC 2.7.1.109) - rat
N:Contains: [acetyl-CoA carboxylase] kinase (EC 2.7.1.128); [hydroxymethylglutaryl-CoA x
C:Species: Rattus norvegicus (Norway rat)
C>Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 05-Oct-2004
C:Accession: A53621; S53729
R:Carling, D.; Aguan, K.; Woods, A.; Verhoeven, A.J.M.; Beri, R.K.; Brenman, C.H.; Sidel
J. Biol. Chem. 269, 11442-11448, 1994
A:Title: Mammalian AMP-activated protein kinase is homologous to yeast and plant protein
A:Reference number: A53621; MUID:94209324; PMID:7908907
A:Accession: A53621
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-552 <CAR>
A:Cross-references: UNIPROT:Q09137; UNIPARC:UPI00001250AB; GB:229486; NID:9488375; PIDN:
R:Gao, G.; Widmer, J.; Stapleton, D.; Teh, T.; Cox, T.; Kemp, B.E.; Watters, L.A.
Biochim. Biophys. Acta 1266, 73-82, 1995
A:Title: Catalytic subunits of the porcine and rat 5'-AMP-activated protein kinase are m
A:Reference number: S53729; MUID:95234757; PMID:7718624
A:Accession: S53729
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-354, 'S', 356-461, 'D', 463-552 <GAO>
A:Cross-references: UNIPARC:UPI00001707CF; GB:U12149; NID:9862472; PIDN:AAA5033.1; PID:
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C:Superfamily: SNF1-related protein kinase; protein kinase homology
C:Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F:14-268/Domain: protein kinase homology <KIN>
F:22-30/Region: protein kinase ATP-binding motif
F:45,64,139,141/Active site: Lys, Glu, Asp, Lys #status predicted
F:144,148/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 18.7%; Score 644; DB 1; Length 552;
Best Local Similarity 43.3%; Pred. No. 1.7e-21;
Matches 139; Conservative 50; Mismatches 116; Indels 16; Gaps 6;

QY 10 YYELHETIGTGGAFAKVLACHILTGEMVAIKMDKNTLGS--DLPRKTEIEALKNLRHQ 67
DB 15 HYLVDGLTGVGTGKVKIGESHQTHGKVAVKILNRQKIRSLDVVGKIKREIQNLKLFRRP 74

QY 68 HICQLYHVLTEANKIFMWLEFCPGGELFDYIIISQDLSEETRVPRQIVSAVAVHSQG 127

DB 75 HIILKLVQVISTPTDFWMVEYSGGELFDYICKGRVEVEARRLFFQQLSAVDYCHRRM 134

QY 128 YAHRLDKPENLLDEYHKLKLDIFGLCAKPKGNKDYHLQTCGSLAYAAPELIQGSYLG 187

DB 135 VVRDLKPEVLLDAHNAKIADFGLSNMMSDGE--FLRTSCGSPNYAAPEVISGRLYAG 192

QY 188 SEADVWSMGLLYVLMCGFLPDDNNMVALYKKIMRGKYDVPKWLSPSSILLLOQMLOYD 247

DB 193 PEVDIWSGCVILYALLCGTLPDDHVPFLFKIRGGVFYIPEYLNRSVATLLMHMLQYD 252

QY 248 PKKRISMKNLNHPWIMQD---YNYPVWQSKNPFTH---LDDDCVTELSVHHR-NNRQT 300

DB 253 PLKRATIKDIRHEWFKQDLPVSLFP-----EDPSYDANVIDEAVKEVCEKPECTESEV 307

QY 301 MEDLISLMQYDHLTATYLLLL 321

DB 308 MNSLYSGDPQDLAVAYHLII 328

RESULT 11
T10449
probable serine/threonine-specific protein kinase (EC 2.7.1.-) - cucumber
N:Alternate names: SNF1-related protein kinase
C:Species: Cucumis sativus (cucumber)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-Oct-2004
C:Accession: T10449
R:Gumpel, N.J.
submitted to the EMBL Data Library, December 1996
A:Reference number: Z17020
A:Accession: T10449
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-504 <GUM>
A:Cross-references: UNIPROT:P93113; UNIPARC:UPI000004B92; EMBL:Y10036
A:Experimental source: cv. Masterpiece; cotyledon
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
C:Superfamily: SNF1-related protein kinase; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:6-260/Domain: protein kinase homology <KIN>

Query Match 18.6%; Score 641.5; DB 2; Length 504;
Best Local Similarity 42.2%; Pred. No. 2e-21;
Matches 146; Conservative 53; Mismatches 102; Indels 45; Gaps 9;

QY 11 YYELHETIGTGGAFAKVLACHILTGEMVAIKMDKNTLGS-DL-PRKTEIEALKNLRHQ 68

DB 8 YKLGKTLGIGSGFKVKAIEHALTGKVAIKILNRKIKMLDMEEKVRRRIKILRLFMHPH 67

QY 69 ICQLYHVLTEANKIFMWLEFCPGGELFDYIIISQDLSEETRVPRQIVSAVAVHSQY 128

DB 68 IIRLYEVIETPSDIYVMVEYKSGELFDYIVKGRLOEDEARNFFQIISGVVEYCHRMV 127

QY 129 AHRDLKPEVLLDEYHKLKLDIFGLCAKPKGN--KDYH-LQTCGSLAYAAPELIQGSY 185

DB 128 VVRDLKPEVLLDSCNKVIADFGI-----SNIMRDGHFLKTCGSPNYAAPEVISGKLY 182

QY 186 LGSEADVWSMGLLYVLMCGFLPDDNNMVALYKKIMRGKYDVPKWLSPSSILLLOQMLO 245

DB 183 AGPEVDVWSGCVILYALLCGTLPDDENIPNLFKIKGIIYLPSSLSSGARELIFPSMLV 242

QY 246 VDPKKRISMKNLNHPWI-----MQDYNYPVWQSKNPFTHLDDDCVTE 290

DB 243 VDPMKRITTEIPRQHPWFOAHLPRYLAVPPDPMQ-----QAKK-----IDEDILQEV 290

QY 291 SVHHRNRRQTMEDLISLMQYDHLTATYLLLLAKKARGKPVRLRSS 336

DB 291 VKMGFDRNLQVSLNRRIQNEATVAYLLL-----DNRPRVSS 328

RESULT 12
T07415
probable serine/threonine-specific protein kinase (EC 2.7.1.-) PKIN1 - potato

N;Alternate names: SNF1-related protein kinase
C;Species: Solanum tuberosum (potato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 05-Oct-2004
C;Accession: J07415
R;Halford, N.G.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z16022
A;Accession: T07415
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-504 <HAL>
A;Cross-references: UNIPROT:Q41485; UNIPARC:UPI00000A0B88; EMBL:X95997; NID:g1216279; P
C;Genetics:
A;Gene: PKINI
A;Introns: 62/1; 123/3; 184/3; 228/3; 290/3; 320/3; 348/3; 389/3; 466/3
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;15-269/Domain: protein kinase homology <KIN>
Query Match 18.6%; Score 640.5; DB 2; Length 504;
Best Local Similarity 42.5%; Pred. No. 2.2e-21;
Matches 136; Conservative 60; Mismatches 111; Indels 13; Gaps 6;
C;QY 8 LKYYELHETIGTGGFAKVKLACHILTGEMVAIKIMDKNTLGS-DL-PRIKTEIEALKNLR 65
D; 14 LRNVGVKTLGHGSGFKVIAEHLTGKVAIKILNRKMKTPDMEKLRREIKICRLFV 73
QY 66 HQHICOLYHVLETKANKIFWVLEYCPGELFDYIISQDLSEETRVVFRQIVSAVYVHS 125
D; 74 HPVIRILEYVETPTDIYVMYVSGELFDYIVKGRLOEDBARKIFQIIGVYCHK 133
QY 126 QGYAHRDLKPENLLFDEYHKLLIDFGLCAKPKGN--KDYH-LQTCGSLAYAAPEL 182
D; 134 NVVHRDLKPENLLDARRNVKIADFGL-----GNIMRDGHFLKTCGSPNYAAPEVSG 188
QY 183 KSYLGSEADVMSGILLYLMCGFLPDDNNVALYKIMRGKYDVPKMLSPSSILL 242
D; 189 KLYAGPEVDVMSGVLVYALLCGTLFPDDENIPNLFKKIKSGVVTLPShLSPLARDLIPR 248
QY 243 MLOVDPKKRISMKNLNHPHPI---MDYNYFVWQSKNPFIIHLDDCVTELShVHNRQ 299
D; 249 MLIVDPKMRISVPIRQHFHLPYLAAPPDPARQHLKLDSEILQVSRMGLDROQ 308
QY 300 TMEDLISLWOYDHLATYLL 319
D; 309 LLDSLQRIQDDATVAYLL 328
RESULT 13
JC1446
serine/threonine-specific protein kinase (EC 2.7.1.-) AK21 - Arabidopsis thaliana
N;Alternate names: protein kinase SNF1 homolog
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Oct-2004
C;Accession: J01446; S58266; S66334
R;LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M.
Gene 120, 249-254, 1992
A;Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protein
A;Reference number: JC1446; MUID:93013041; PMID:1339373
A;Accession: JC1446
A;Molecule type: DNA
A;Residues: 1-512 <LEG>
A;Cross-references: UNIPROT:Q38997; UNIPARC:UPI000012DE43; GB:M93023; NID:g166599; PIDN:
R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Ditttrich, P.
submitted to the EMBL Data Library, May 1995
A;Description: Differential accumulation of the transcripts of 22 novel protein kinase g
A;Reference number: S58266
A;Accession: S58266
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 144-198 <THU>

A;Cross-references: UNIPARC:UPI000009DEB0; EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PII
R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Ditttrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A;Title: Differential accumulation of the transcripts of 22 novel protein kinase genes in
A;Reference number: S66314; MUID:96123233; PMID:8534852
A;Accession: S66334
A;Molecule type: DNA
A;Residues: 144-198 <TH2>
A;Cross-references: UNIPARC:UPI000009DEB0; EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PII
C;Comment: This enzyme plays an important role in a signal transduction cascade regulatir
C;Genetics:
A;Gene: AKin10; AK21
A;Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;17-271/Domain: protein kinase homology <KIN>
F;25-33/Region: protein kinase ATP-binding motif
F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Aen, Asp) #status predicted
Query Match 18.5%; Score 637; DB 1; Length 512;
Best Local Similarity 38.8%; Pred. No. 3.2e-21;
Matches 151; Conservative 61; Mismatches 133; Indels 44; Gaps 11;
C;QY 5 DELKTYELHETIGTGGFAKVKLACHILTGEMVAIKIMDKNTLGS--DLPRIKTEIEALK 62
D; 13 ESILPNYKLGRTIGSGFGRVIAEHALTGKVAIKILNRKIKNMEEKVREIKILR 72
QY 63 NLRHQHICOLYHVLETKANKIFWVLEYCPGELFDYIISQDLSEETRVVFRQIVSAVAY 122
D; 73 LFMHPHIIILYEVETPTDIYVMYVSGELFDYIVKGRLOEDBARNFQQIISGVEY 132
QY 123 VHSQGYAHRDLKPENLLFDEYHKLLIDFGLCAKPKGN--KDYH-LQTCGSLAYAAPEL 179
D; 133 CHRNWVHRDLKPENLLDSCNVKIADFGL-----SNIMRDGHFLKTCGSPNYAAPEV 187
QY 180 IQGKSYLGSEADVMSGILLYLMCGFLPDDNNVALYKIMRGKYDVPKMLSPSSILL 239
D; 188 ISGLYAGPEVDVMSGVLVYALLCGTLFPDDENIPNLFKKIKGGIYTLPSHLSPGARDL 247
QY 240 LQOMLOVDPKKRISMKNLNHPHPI---MDYNYFVWQSKNPFIIHLDDCVTEL 290
D; 248 IPRMLVDPKMRISVPIRQHFHLPYLAAPPDPDPVQQAQK----IDEEILQEV 301
QY 291 SVHHRNRNQTMEDLISLWOYDHLATYLLAKKARGKPVRLRLSSFSFGQ----QASAT 345
D; 302 INMGFDRNHLIESLRNTQDGTVTYYLIDN-----RFRASSGYLGAEFQETWEGT 353
QY 346 PFTDIKSNNSWLEDVTASDKNTYVAGLIDY 374
D; 354 P-----RMHPAESVASPVSHRLPGLMEY 376
RESULT 14
S60304
serine/threonine-specific protein kinase (EC 2.7.1.-) BKIN12 (version 2) - barley
C;Species: Hordeum vulgare (barley)
C;Date: 19-Mar-1997 #sequence_revision 15-Aug-1997 #text_change 05-Oct-2004
C;Accession: S60304; S24579
R;Halford, N.G.; Vicente-Carabajosa, J.; Sabelli, P.A.; Shewry, P.R.; Hammappel, U.; Kreis
Plant J. 2, 791-797, 1992
A;Title: Molecular analyses of a barley multigene family homologous to the yeast protein
A;Reference number: S60303; MUID:93258420; PMID:1302632
A;Accession: S60304
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-513 <HAL>
A;Cross-references: UNIPROT:Q40030; UNIPARC:UPI000017255D; EMBL:X65604
R;Halford, N.G.
submitted to the EMBL Data Library, April 1992
A;Reference number: S24578

A;Accession: S24579
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-61, 'A', '63-513 <HA2>
A;Cross-references: UNIPARC:UPI00000A3F6F; EMBL: X65604; NID: g18933; PIDN: CAA46554.1; PID
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;15-272/Domain: protein kinase homology <KIN>
F;23-31/Region: protein kinase ATP-binding motif
F;46,65,143,145/Active site: Lys, Glu, Asp, Lys #status predicted
F;148,152/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 18.5%; Score 637; DB 1; Length 513;
Best Local Similarity 39.4%; Pred. No. 3.2e-21;
Matches 152; Conservative 64; Mismatches 136; Indels 34; Gaps 10;

QY 4 YDELLKYELHETIGTGFAKVKLACHILTGEMVAIKIMDKNTLGSGLPRIK--TEIEAL 61
DB 10 HSEVLKYNLKGTLGLGTFGDVKAERNVTGQVAKILNRRKMETWEMEKEGNRIKIM 69

QY 62 K---NLRHQHI COLYHVLETANKIFMWLEVCYCGELFDYIIISODRLSEEBETRVVFRQIVS 118
DB 70 RLFDITPHPIIRVYEIVETPKDIFVVMVEYCNNGELLDYIIENGRLQDEARRIFQOILA 129

QY 119 AVAVHSQGYAHRDLKPENLLFDEYHKLKLIDFGLCAKPKGNKDYH-LQTCGSLAYAAP 177
DB 130 GVEYCHRMVVRDLKPENLLDSRYNVKLDLFGF---SNVMDGHFLKTS CGSLNAYAP 186

QY 178 ELIQGSKYLGSEADVMSGILLYVLMCGFLPFDDDNVMALYKKIMRGKYDVPKWLSPSSI 237
DB 187 EIISSKLYAGPEVDVMSGVLVALLCGSVFPDDNIPSLFKIKGGTYILPSYLSDSAR 246

QY 238 LLLQQLQVDPKPKRISMKNLNHPWIMQDYNYPV-----EWQSKNPFHLLDDCVT 288
DB 247 DLIPKLNIDPMKRITFHEIRVHPFKN--HLPCLYAVPPPYKEQQAQ---MIDEDILR 300

QY 289 ELSVHRRNRQTMEDLISLWQDHLTATYLLAKKARGKPVRLRLSSFCGQASATPFT 348
DB 301 EYVNLGYDKDHVCESLWNRLQNEETVAYILL-----DDRFRTSGYL-G-ADHQHLM 351

QY 349 DIKSNWMSL-EDVTASDKNYVAGLID 373
DB 352 DRSFNEFTLSASASPTENVLPGLND 377

RESULT 15
S72513
FOG2 protein - yeast (Kluyveromyces marxianus var. lactis)
C;Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
C;Date: 29-Jan-1998 #sequence revision 06-Feb-1998 #text change 05-Oct-2004
R;Accession: S72513
R;Goffrini, P.; Ficarella, A.; Donnini, C.; Lodi, T.; Puglisi, P.P.; Ferrero, I.
Curr. Genet. 29, 316-326, 1996
A;Title: FOG1 and FOG2 genes, required for the transcriptional activation of glucose-rep
A;Reference number: S72513; MUID: 96171514; PMID: 8598052
A;Accession: S72513
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-602 <GOF>
A;Cross-references: UNIPROT: P87209; UNIPARC: UPI000006A88D
A;Note: the source is designated as Kluyveromyces lactis
C;Genetics:
A;Gene: FOG2
C;Function:
A;Description: probably involved in the regulation of glucose-repressible gene expressio
C;Superfamily: SNF1-related protein kinase; protein kinase homology
F;33-286/Domain: protein kinase homology <KIN>

Query Match 18.5%; Score 636; DB 2; Length 602;
Best Local Similarity 44.5%; Pred. No. 4.1e-21;
Matches 133; Conservative 51; Mismatches 87; Indels 28; Gaps 7;

QY 11 YELHETIGTGFAKVKLACHILTGEMVAIKIMDKNTLGSGLPRIK--TEIEALKNLRHQH 68
DB 35 YQIITLGGSGFGVKLAHYHISTGQKVALKIINKKVLAKSDMQGRIEREISYLRLLRHPH 94

QY 69 ICQLYHVLETANKIFMWLEVCYCGELFDYIIISODRLSEEBETRVVFRQIVSNAVYHSQGY 128
DB 95 IIKLYDVIKSDEIIMVIEYA-GNELFDYIVQDKMPEQEARFFQOIISAVDYCHRHKI 153

QY 129 AHRDLKPENLLFDEYHKLKLIDFGLC-AKPKGNKDYHLOTCCGSLAYAAPLTIQKSYLG 187
DB 154 VHRDLKPENLLLDEHLNVLKIDFGLSNIMTDGN---FLKTS CGSPNYAAPEVISGKLYAG 210

QY 188 SEADVMSGILLYVLMCGFLPFDDDNVMALYKKIMRGKYDVPKWLSPSSI LLLQQLQV 247
DB 211 PEVDVMSGVLVLMCGFLPFDDNIPSLFKIKGGTYILPSYLSDSAR 270

QY 248 PKKRISMKNLNHPWIMQDYNYPV-----EWQSKNPFHLLDDCVT ELSVHRRNRQTMED 303
DB 271 PVNRI TVHEIMQDEWPKVDLPDYLPAAE-----STHQENSESKTED 311

Search completed: November 21, 2006, 14:14:15
Job time : 47 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: November 21, 2006, 14:13:40 ; Search time 53 Seconds
(without alignments)
1075.140 Million cell updates/sec

Title: US-10-656-598-2
Perfect score: 3447
Sequence: 1 MKDYDELLKYYELHETIGT.....KGDWVYKRLVEDILSSCKV 651

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SID33/ptodata/2/iaa/5 COMB.pap.*
- 2: /EMC_Celerra_SID33/ptodata/2/iaa/5 COMB.pap.*
- 3: /EMC_Celerra_SID33/ptodata/2/iaa/7 COMB.pap.*
- 4: /EMC_Celerra_SID33/ptodata/2/iaa/H COMB.pap.*
- 5: /EMC_Celerra_SID33/ptodata/2/iaa/PCITUS COMB.pap.*
- 6: /EMC_Celerra_SID33/ptodata/2/iaa/RE COMB.pap.*
- 7: /EMC_Celerra_SID33/ptodata/2/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3447	100.0	651	2	US-09-870-937-10
2	791.5	23.0	724	2	US-09-949-016-8234
3	789.5	22.9	713	2	US-09-538-092-1022
4	789.5	22.9	713	2	US-09-949-016-6214
5	788.5	22.9	729	1	US-08-677-298-2
6	788.5	22.9	729	2	US-09-523-849-33
7	770.5	22.4	691	2	US-09-949-016-8255
8	770.5	22.4	691	2	US-09-949-016-8256
9	769.5	22.3	724	2	US-09-984-890-2
10	769.5	22.3	724	2	US-10-274-194-2
11	769.5	22.3	724	2	US-10-760-407-2
12	764.5	22.2	745	2	US-09-523-849-36
13	759.5	22.0	722	2	US-09-984-890-4
14	759.5	22.0	722	2	US-10-274-194-4
15	759.5	22.0	722	2	US-10-760-407-4
16	754.5	21.9	722	2	US-08-817-832B-32
17	742.5	21.5	793	2	US-09-523-849-32
18	724.5	21.0	779	2	US-08-817-832B-31
19	669	19.4	557	2	US-09-949-016-10174
20	668.5	19.4	602	2	US-09-949-016-7417
21	668.5	19.4	602	2	US-09-949-016-7418
22	665.5	19.3	345	2	US-09-101-146-1
23	654	19.0	832	2	US-10-464-939-2
24	653	18.9	1058	2	US-10-464-939-4
25	644	18.7	552	2	US-08-557-006C-40
26	642	18.6	257	2	US-09-101-146-6

ALIGNMENTS

RESULT 1

US-09-870-937-10
; Sequence 10, Application US/09870937

; Patent No. 6974867

; GENERAL INFORMATION:

; APPLICANT: Wu, Bin

; APPLICANT: Seeley, Todd

; APPLICANT: Williams, Lewis T.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEOPLASTIC DISEASE USING CHEMOTHERAPY AND RADIATION SENSITIZERS

; FILE REFERENCE: 200130.514/PP-01623.002

; CURRENT APPLICATION NUMBER: US/09/870,937

; CURRENT FILING DATE: 2001-05-30

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 10

; LENGTH: 651

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-870-937-10

Query Match	100.0%;	Score 3447;	DB 2;	Length 651;
Best Local Similarity	100.0%;	Pred. No. 2.4e-310;		
Matches 651;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MKDYDELLKYYELHETIGTGGPAKVKLACHILTGMVAIKIMDKNTLGSDDLPRIKTEIEA	60	
DB	1	MKDYDELLKYYELHETIGTGGPAKVKLACHILTGMVAIKIMDKNTLGSDDLPRIKTEIEA	60	
QY	61	LKNTLHQHICQLYHYLTANKIFMWLEVCPCGELDYIISODRLSEETRVVFRQIVSAV	120	
DB	61	LKNTLHQHICQLYHYLTANKIFMWLEVCPCGELDYIISODRLSEETRVVFRQIVSAV	120	
QY	121	AYVHSQGVYAHRLDKPENLLFDEYHKLKLDLFGLCAPKGNKDYHLQTCGSLAYAAPELI	180	
DB	121	AYVHSQGVYAHRLDKPENLLFDEYHKLKLDLFGLCAPKGNKDYHLQTCGSLAYAAPELI	180	
QY	181	QKSYLGSSEADVWSMGIILLYVLMCGFLPFDDNNVALYKIMRGKYDVDPKWLSPSSILL	240	
DB	181	QKSYLGSSEADVWSMGIILLYVLMCGFLPFDDNNVALYKIMRGKYDVDPKWLSPSSILL	240	
QY	241	QOMLVDPKRIKIMKVNLLNHPIMQDYNYPVWQSKNPFHLLDDCVTELSSHNNRQT	300	
DB	241	QOMLVDPKRIKIMKVNLLNHPIMQDYNYPVWQSKNPFHLLDDCVTELSSHNNRQT	300	
QY	301	MEDLISLWQYDHLTATYLLLLAKARGKPVRLRLSSFCGQASATPFTDIKSNWLSDEV	360	
DB	301	MEDLISLWQYDHLTATYLLLLAKARGKPVRLRLSSFCGQASATPFTDIKSNWLSDEV	360	

QY 361 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
DB |||||
361 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
QY 421 KKNENYVTPKSAVKNBEYFMPEPKTPVKNQKHREILTPNRYTTPSKARNQCLKETPI 480
DB |||||
421 KKNENYVTPKSAVKNBEYFMPEPKTPVKNQKHREILTPNRYTTPSKARNQCLKETPI 480
QY 481 KIPVNSTGDKLMTGTVISPERCRSVELDLNOAHMEETPKRGAKEVFGSLERGLDKVIIV 540
DB |||||
481 KIPVNSTGDKLMTGTVISPERCRSVELDLNOAHMEETPKRGAKEVFGSLERGLDKVIIV 540
QY 541 LTRSKKGSARDGPRRLKHLHYNTTTRLVNPDQLNEIMSLPKKHVDVQKGYTLKCO 600
DB |||||
541 LTRSKKGSARDGPRRLKHLHYNTTTRLVNPDQLNEIMSLPKKHVDVQKGYTLKCO 600
QY 601 QSDFGKVTWQFELEVCOQKPDVVGIRRLKGDAMVYKRLVEDILSSCKV 651
DB |||||
601 QSDFGKVTWQFELEVCOQKPDVVGIRRLKGDAMVYKRLVEDILSSCKV 651
RESULT 2
US-09-949-016-8234
; Sequence 8234, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8234
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8234

Query Match 23.0%; Score 791.5; DB 2; Length 724;
Best Local Similarity 30.7%; Pred. No. 3.8e-64;
Matches 217; Conservative 121; Mismatches 254; Indels 115; Gaps 21;
QY 11 YELHETIGTGGAFAKVKLACHILTGEMVAIKIMDKNTLG-SDLPRIKTEIEALKNLRHQHI 69
DB |||||
67 YRLKTKIGKGNFAKVKLARHILTGREVAIKIIDKTQLNPTSLOKLPREVIRIMKILNHPNI 126
QY 70 COLYHLETANKIFMVLEYCPGELFDYIISQDRLSEETRVVFRQIVSAVAVHVSQGYA 129
DB |||||
127 VKLFEVIEQTKLYLIMEVAGSEVFDYLVAGRMKEKARSKEFQIVSAVQYCHQKRIV 186
QY 130 HRDLKPENLLFDEYHKLKIDFGLCAK-PKGNKDYHLQTCGSLAYAAPELQKGYLGS 188
DB |||||
187 HRDLKAENLLDADNMNIKIADFGSNEFTVGK--LDTPCGSPPPYAAPELFGKKYDGP 243
QY 189 EADVMSGILLVLMCGFLPPDDNNVMALYKKIMRGKYDVPKWLSPSSILLQOQLQVDP 248
DB |||||
244 EVDVMSGLVILTYLVSGSLPFDGQNLKELRERVLRGKIRPIPFYMSDTCENLLKRFVLVLP 303
QY 249 KGISMKNLNHPWIMQDYNYPVWQSKNPFIFH----LDDCVTELSVHRNNRQTMEDL 304
DB |||||
304 IKGTLQEQIMKDRWI---NAGHEEDELKPFVEPELDISQKRIDIMVGVNGYQEBIQES 359
QY 305 ISLWQYDHLTATYLLLLAKARQKPVRLRLSSFCGQASATPTFDI-----KSNWWS 356
DB |||||
360 LSKMKTDEITATYLLLLGRKSSVRP-----SSDLNNSGTQSPHHKVRQSVSSQKORRYS 414

QY 357 -----LBDVTASDKNYVAGLIDYDWCDDDLST-----GAATP- 388
DB |||||
415 DHAGPAIFSVVAYPKRSQTSADSDLKEDGIGSSRRKSSGSAVGGKGIAPASPMLGNASPN 474
QY 389 -----RTSQFTKYWTESNGVESKSLTPALCRTPANKLKNKENVYTPKSAVKN-EEYF 439
DB |||||
475 KADIPERKKSSTVPSSNTASGWMTRNTYVCSERTADR-----HSVIQNGKENS 524
QY 440 MPEPKTPVKNQKHREILTPNRYTTPSKARNQCLKETPIKIPVNSTGDKLMTGVIIV 499
DB |||||
525 TIPDQRTPV-ASTHISIAAATPDR-----IRFP--RGTASRSTFHQGP 564
QY 500 -ERRC-----RSVELDLNOAHMEETPKRGAKEVFGSLERGLDKVIIVLTRSK-----R 546
DB |||||
565 RERRATYNGPPASPSSLSHEATPLSQTRSGSTNLF-----SKLTSKLTFRSNVSAEQ 617
QY 547 KGSARDG-PRRLKHLHYNTTTRLVNPDQLNEIMSLPKKHVDVQK-GYTLKCOQSD 604
DB |||||
618 KDNKEAKPRSLRFTWSMKTTSSMDPGDMREIRKVLDAANNCDYERQERFLLFCVHGDGH 677
QY 605 GKVTWQFELEVCOQKPDVVGIRRLKGDAMVYKRLVEDILSSCKV 651
DB |||||
678 AENLVQWEMEVECKLPRLSLNGVRFKRISGTSIAFKNIASKIANELKL 724

RESULT 3
US-09-538-092-1022
; Sequence 1022, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqformatter Version 0.9
; SEQ ID NO 1022
; LENGTH: 713
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P27448
US-09-538-092-1022

Query Match 22.9%; Score 789.5; DB 2; Length 713;
Best Local Similarity 30.6%; Pred. No. 5.6e-64;
Matches 217; Conservative 119; Mismatches 254; Indels 119; Gaps 22;
QY 11 YELHETIGTGGAFAKVKLACHILTGEMVAIKIMDKNTLG-SDLPRIKTEIEALKNLRHQHI 69
DB |||||
56 YRLKTKIGKGNFAKVKLARHILTGREVAIKIIDKTQLNPTSLOKLPREVIRIMKILNHPNI 115
QY 70 COLYHLETANKIFMVLEYCPGELFDYIISQDRLSEETRVVFRQIVSAVAVHVSQGYA 129
DB |||||
116 VKLFEVIEQTKLYLIMEVAGSEVFDYLVAGRMKEKARSKEFQIVSAVQYCHQKRIV 175
QY 130 HRDLKPENLLFDEYHKLKIDFGLCAK-PKGNKDYHLQTCGSLAYAAPELQKGYLGS 188
DB |||||
176 HRDLKAENLLDADNMNIKIADFGSNEFTVGK--LDTPCGSPPPYAAPELFGKKYDGP 232
QY 189 EADVMSGILLVLMCGFLPPDDNNVMALYKKIMRGKYDVPKWLSPSSILLQOQLQVDP 248
DB |||||
233 EVDVMSGLVILTYLVSGSLPFDGQNLKELRERVLRGKIRPIPFYMSDTCENLLKRFVLVLP 292

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-677-298-2

Query Match 22.9%; Score 788.5; DB 1; Length 729;
Best Local Similarity 30.0%; Pred. No. 7.2e-64;
Matches 216; Conservative 124; Mismatches 256; Indels 123; Gaps 20;

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QY 11 YELHETIGTGGFAKVKLACHILTGEMVAIKIMDKNTLG-SDLPRIKTEIEALKNLRHOHI 69
DB 56 YRLKTIKGKGNFAKVKLARHILTGREVAIKIDKTLQNLPTSQKLFREVRIMKILNHPNI 115
QY 70 COLYHVLETANKIFMWLEYPGGELEFDYIIISODRLSEEBETRVVFRQIVSAVAVHSQGYA 129
DB 116 VKLFEVIEKTEKTYLIMEYASGGEVFDYLVAGHRMKEARSKFRQIVSAVQYCHQKRV 175
QY 130 HRDLKPENLLFDYHKLKIDIFGLCAK-PKGNKYHLOTCCGSLAYAAPELIQKSYLGS 188
DB 176 HRDLKAENLLDADNMNIADFGSNEFTVGK---LDTFCGSPPYAAPELFGKKYDGP 232
QY 189 EADVWSMGLLYVLMCGFLPDDDDNMALYKIMRGKYDVPKWLSPSSILLQQMLQVDP 248
DB 233 EVDVWSGLVILYTLVSGSLPFDGQNLKELRERVLRGKRIIPFYMSTDCENLLKRLFLVLP 292
QY 249 KKRISMKNLNHPIMQDYNYPVEMQSKNPFTH---LDDDCVTELSVHHRNNRQTMEDL 304
DB 293 IKRGTELEQIMKORNI---NAGHEEDELKPFVEPELDISDOKREIDIMVGMGYSQEBIQES 348
QY 305 ISLMQYDHLTATYLLLLAKKARGKVPRLRLSFSQCOASATPTDIKSNW----- 355
DB 349 LSKMKYDEITATY-LLGKRKSELSDASDSSSSNLSLAKVRPSSDLNNSGQSPHHKVQR 407
QY 356 -----SLEDVTASDKNYVAGLIDYDWCEDDLST----- 383
DB 408 SVSSSQKORRYSDHAGPAIPSVVAYPKRSQTSADGDLKEDGISRKSXSGS VGGKIAP 467
QY 384 -----GAATP-----RTSQTKYWTESNGVESKSLTPALCRTPANKLNKNENVT 428
DB 468 ASPMLGNASNPNKADIPERKKSSTVPSSNTASGGMTRNTYVCSERTADR----- 518
QY 429 PKSAYKN-BEYFMPPEKTPVKNQKHREILTPNRYTTPSKARNOCLKETPIKIPVNST 487
DB 519 -HSVIONGKENSTIPDQRTPV-ASTHSISSAATPDR-----IRFP---R 557
QY 488 GTDKLMTGVISP-ERRC-----RSVELDLNQAHEETPKRGAKVFGSLERGLDKVIT 539
DB 558 GTASRSTFHGQPRERTATYNGPPSPSLSHEATPLSOTRSRGSTNLF-----SKLTS 610
QY 540 VLTRSK-----RKGSGARDG-PRRLKLYNVTTTLLVNPDLNLEIMSLPKKHVDFVQK- 592
DB 611 KLTRSRNVSAEQDENKEAKPRSLRFTWSMKTSSMDPGDMREIRKVLNANNCDEYQRE 670
QY 593 GYTLKQOTQSDFGKVTMQFEVLCQKPDVVGIRQRQLKGDWVYKRLVEDILSSCKV 651
DB 671 RPLLCVHGDAENLVQMEMEVCKLPRLSLNGVRFKRIISGTSIAFNKIASIANELKL 729
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RESULT 6

US-09-523-849-33
; Sequence 33, Application US/09523849
; Patent No. 6458561
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Molteni, Angela
; APPLICANT: Magnagni, Paola
; APPLICANT: Bosotti, Roberta
; APPLICANT: Scacheri, Emanuela
; APPLICANT: Isacchi, Antonella
; APPLICANT: Hodgson, Dave
; TITLE OF INVENTION: HUMAN NIMI KINASE
; FILE REFERENCE: PC-0009 US
; CURRENT APPLICATION NUMBER: US/09/523,849

; CURRENT FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank Accession No. 6458561 g3089349
US-09-523-849-33

Query Match 22.9%; Score 788.5; DB 2; Length 729;
Best Local Similarity 30.0%; Pred. No. 7.2e-64;
Matches 216; Conservative 124; Mismatches 256; Indels 123; Gaps 20;

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QY 11 YELHETIGTGGFAKVKLACHILTGEMVAIKIMDKNTLG-SDLPRIKTEIEALKNLRHOHI 69
DB 56 YRLKTIKGKGNFAKVKLARHILTGREVAIKIDKTLQNLPTSQKLFREVRIMKILNHPNI 115
QY 70 COLYHVLETANKIFMWLEYPGGELEFDYIIISODRLSEEBETRVVFRQIVSAVAVHSQGYA 129
DB 116 VKLFEVIEKTEKTYLIMEYASGGEVFDYLVAGHRMKEARSKFRQIVSAVQYCHQKRV 175
QY 130 HRDLKPENLLFDYHKLKIDIFGLCAK-PKGNKYHLOTCCGSLAYAAPELIQKSYLGS 188
DB 176 HRDLKAENLLDADNMNIADFGSNEFTVGK---LDTFCGSPPYAAPELFGKKYDGP 232
QY 189 EADVWSMGLLYVLMCGFLPDDDDNMALYKIMRGKYDVPKWLSPSSILLQQMLQVDP 248
DB 233 EVDVWSGLVILYTLVSGSLPFDGQNLKELRERVLRGKRIIPFYMSTDCENLLKRLFLVLP 292
QY 249 KKRISMKNLNHPIMQDYNYPVEMQSKNPFTH---LDDDCVTELSVHHRNNRQTMEDL 304
DB 293 IKRGTELEQIMKORNI---NAGHEEDELKPFVEPELDISDOKREIDIMVGMGYSQEBIQES 348
QY 305 ISLMQYDHLTATYLLLLAKKARGKVPRLRLSFSQCOASATPTDIKSNW----- 355
DB 349 LSKMKYDEITATY-LLGKRKSELSDASDSSSSNLSLAKVRPSSDLNNSGQSPHHKVQR 407
QY 356 -----SLEDVTASDKNYVAGLIDYDWCEDDLST----- 383
DB 408 SVSSSQKORRYSDHAGPAIPSVVAYPKRSQTSADGDLKEDGISRKSXSGS VGGKIAP 467
QY 384 -----GAATP-----RTSQTKYWTESNGVESKSLTPALCRTPANKLNKNENVT 428
DB 468 ASPMLGNASNPNKADIPERKKSSTVPSSNTASGGMTRNTYVCSERTADR----- 518
QY 429 PKSAYKN-BEYFMPPEKTPVKNQKHREILTPNRYTTPSKARNOCLKETPIKIPVNST 487
DB 519 -HSVIONGKENSTIPDQRTPV-ASTHSISSAATPDR-----IRFP---R 557
QY 488 GTDKLMTGVISP-ERRC-----RSVELDLNQAHEETPKRGAKVFGSLERGLDKVIT 539
DB 558 GTASRSTFHGQPRERTATYNGPPSPSLSHEATPLSOTRSRGSTNLF-----SKLTS 610
QY 540 VLTRSK-----RKGSGARDG-PRRLKLYNVTTTLLVNPDLNLEIMSLPKKHVDFVQK- 592
DB 611 KLTRSRNVSAEQDENKEAKPRSLRFTWSMKTSSMDPGDMREIRKVLNANNCDEYQRE 670
QY 593 GYTLKQOTQSDFGKVTMQFEVLCQKPDVVGIRQRQLKGDWVYKRLVEDILSSCKV 651
DB 671 RPLLCVHGDAENLVQMEMEVCKLPRLSLNGVRFKRIISGTSIAFNKIASIANELKL 729
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RESULT 7

US-09-949-016-8255
; Sequence 8255, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8255
LENGTH: 691
TYPE: PRT
ORGANISM: Human
US-09-949-016-8255

Query Match 22.4%; Score 770.5; DB 2; Length 691;
Best Local Similarity 30.5%; Pred. No. 3.1e-62;
Matches 219; Conservative 123; Mismatches 252; Indels 125; Gaps 24;

QY 11 YELHETIGTGFAKVKLACHILITGEMVAIKIMDKNTL-GSDLPRIKTEALKNLHQHI 69
Db 20 YRLKTIKGNFAKVKLARHILITGKEVAVKIIDKTLNSSLQKLFREVRIMKVLNHPNI 79
QY 70 CQLYHVLETANKIFMWLEPCGELFDYIISODRLSEETRVVFRQIVSAVAVHSGYA 129
Db 80 VKLFEVETETKLYLMEVAGSGEVDYLAHGRMEKEARAKFRQIVSAVQYCHQKFTV 139
QY 130 HRDLKPNILFDYHKLIDFGLCAK-PKGNKYHLOTCCGSLAAYAAPELQKSYLGS 188
Db 140 HRDLKAENLLDADNMKIADFGNEFTGNK---LDTFCGSPPYAAPELFGKKYDGP 196
QY 189 EADVSMGILLYVLMCGELPFDDNNMALKYKIMRGKYDVPKWLSPSSILLQOMLVQDP 248
Db 197 EVDVNSGLVILYLVSGSLPFDQNLKELRERVLRGKYRIPFYMSDTCENLLKFKLILNP 256
QY 249 KGRISMKNLNHPIMQDYNYPVWQSKNPFTH---LDDDCVTELSVHHRNNRQTMEDL 304
Db 257 SKRGTELEQIMKDRWM---NVGHEDDELKPYVEPLDYKDPRTTELMSVSMGYTREIIDS 312
QY 305 ISLWQYDHLTATYLLALLAKA--RGPVRL--RLSSFSCGOASATPTDIKSNWNSLEVD 360
Db 313 LVGQRYNEVMATYLLGYKSSLEGGDTITLKPRPSADLTNSSAPSPSHKVQ-----RSV 366
QY 361 TASDKNVAGLIDYDWCEDDLSTGAATPRTSOFTKYWTESNGVESKSLTPALCRTPANKL 420
Db 367 SANPKOR-----RPSDQAGPAIPTSNYSYKK-TQSNNAENK--RPEEDRESGRKA 413
QY 421 KKNENYTPKSAVKNEEYFMPEPTPVNKNQHKREILTPN-----RYTTPSKARNQC 474
Db 414 SSTAKV-----PASPLPGLERKK---TTPPTSTNSVLSTSTNRSRNSP 453
QY 475 LKE-----TPIKIPVNSTGDKMTGVISPER-----R 502
Db 454 LLERASLQASIQNGKSTAPQRPVPSAPSAHNISSSGGAPDRTPPGRVSSRSTFHAQC 513
QY 503 CRSVELDLQAHEETPK-----RKA--KVFGS-----LERGL-----DKVITVL 541
Db 514 LRQVR-DQONLPYGVTPASPSGHSQGRGASGIFSKFTSKFVRRLNLPESKDRVETLR 572
QY 542 T-----RSKRKGSARDG-PRRLKLVNVTTLVNPDLNNEIMSILPKKHVDF-VOK 592
Db 573 PHVVGSGNDKEKEEFREAKPRSLRTWSMKTTSMEPEMREIRKVLNDANSQCSELHE 632
QY 593 GYTLKQCTQSDFGKVTMQELEVQIQDPDVGIRQRKLGDAWVYKRLVEDILSSCKV 651
Db 633 KYMLLCWGHGTGPHEDFVQWMEVCKLPRLSLNGVRFKRISGTSMAFKNIASKIANELKL 691

RESULT 8

US-09-949-016-8256

; Sequence 8256, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8256
LENGTH: 691
TYPE: PRT
ORGANISM: Human
US-09-949-016-8256

Query Match 22.4%; Score 770.5; DB 2; Length 691;
Best Local Similarity 30.5%; Pred. No. 3.1e-62;
Matches 219; Conservative 123; Mismatches 252; Indels 125; Gaps 24;

QY 11 YELHETIGTGFAKVKLACHILITGEMVAIKIMDKNTL-GSDLPRIKTEALKNLHQHI 69
Db 20 YRLKTIKGNFAKVKLARHILITGKEVAVKIIDKTLNSSLQKLFREVRIMKVLNHPNI 79
QY 70 CQLYHVLETANKIFMWLEPCGELFDYIISODRLSEETRVVFRQIVSAVAVHSGYA 129
Db 80 VKLFEVETETKLYLMEVAGSGEVDYLAHGRMEKEARAKFRQIVSAVQYCHQKFTV 139
QY 130 HRDLKPNILFDYHKLIDFGLCAK-PKGNKYHLOTCCGSLAAYAAPELQKSYLGS 188
Db 140 HRDLKAENLLDADNMKIADFGNEFTGNK---LDTFCGSPPYAAPELFGKKYDGP 196
QY 189 EADVSMGILLYVLMCGELPFDDNNMALKYKIMRGKYDVPKWLSPSSILLQOMLVQDP 248
Db 197 EVDVNSGLVILYLVSGSLPFDQNLKELRERVLRGKYRIPFYMSDTCENLLKFKLILNP 256
QY 249 KGRISMKNLNHPIMQDYNYPVWQSKNPFTH---LDDDCVTELSVHHRNNRQTMEDL 304
Db 257 SKRGTELEQIMKDRWM---NVGHEDDELKPYVEPLDYKDPRTTELMSVSMGYTREIIDS 312
QY 305 ISLWQYDHLTATYLLALLAKA--RGPVRL--RLSSFSCGOASATPTDIKSNWNSLEVD 360
Db 313 LVGQRYNEVMATYLLGYKSSLEGGDTITLKPRPSADLTNSSAPSPSHKVQ-----RSV 366
QY 361 TASDKNVAGLIDYDWCEDDLSTGAATPRTSOFTKYWTESNGVESKSLTPALCRTPANKL 420
Db 367 SANPKOR-----RPSDQAGPAIPTSNYSYKK-TQSNNAENK--RPEEDRESGRKA 413
QY 421 KKNENYTPKSAVKNEEYFMPEPTPVNKNQHKREILTPN-----RYTTPSKARNQC 474
Db 414 SSTAKV-----PASPLPGLERKK---TTPPTSTNSVLSTSTNRSRNSP 453
QY 475 LKE-----TPIKIPVNSTGDKMTGVISPER-----R 502
Db 454 LLERASLQASIQNGKSTAPQRPVPSAPSAHNISSSGGAPDRTPPGRVSSRSTFHAQC 513
QY 503 CRSVELDLQAHEETPK-----RKA--KVFGS-----LERGL-----DKVITVL 541
Db 514 LRQVR-DQONLPYGVTPASPSGHSQGRGASGIFSKFTSKFVRRLNLPESKDRVETLR 572
QY 542 T-----RSKRKGSARDG-PRRLKLVNVTTLVNPDLNNEIMSILPKKHVDF-VOK 592
Db 573 PHVVGSGNDKEKEEFREAKPRSLRTWSMKTTSMEPEMREIRKVLNDANSQCSELHE 632
QY 593 GYTLKQCTQSDFGKVTMQELEVQIQDPDVGIRQRKLGDAWVYKRLVEDILSSCKV 651
Db 633 KYMLLCWGHGTGPHEDFVQWMEVCKLPRLSLNGVRFKRISGTSMAFKNIASKIANELKL 691

RESULT 9
US-09-984-890-2
; Sequence 2, Application US/09984890
; Patent No. 6492156
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001306
; CURRENT APPLICATION NUMBER: US/09/984,890
; CURRENT FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-890-2

Query Match 22.3%; Score 769.5; DB 2; Length 724;
Best Local Similarity 30.3%; Pred. No. 4.1e-62;
Matches 218; Conservative 124; Mismatches 252; Indels 125; Gaps 24;

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Qy 11 YELHETIGTGGAFAKVLACHILTGEMVAIKIMDKNTL-GSDLPRIKTEIEALKNLRHQHI 69
Db 53 YRLKKTIGKGNFAKVLARHILTGKEVAVKIIDKTQLNSSLQKLFREVRIMKVLNHPNI 112

Qy 70 COLYHLETANKIFMWLEYPGCGELFDYIISQDRLSEETRVVFRQIVSAVAVVHSGYA 129
Db 113 VKLFEVETETKLYLVMEYASGEVFDYLVAGHMKKEARAKFRQVVSAYVQYCHQKFIV 172

Qy 130 HRDLKPENLLFDYHKLKLIIDFGLCAK-PKGNKYHLQTCGSLAYAAPELIQGSYLS 188
Db 173 HRDLKAENLLDADMNKIADFGSNEFTFGNK---LDTFCGSPPYAAPELFGQKYDGP 229

Qy 189 EADVMSGILLVLMCGFLPFDDNNMALKYKIMRGKYDVPKWLSPSSILLQOQLQVDP 248
Db 230 EVDVMSGLVLYLVSGSLFPDQNLKELREVRVLRGKRIIPFYMTSDCNLKKFILIHP 289

Qy 249 KKRISMKNLNLHPWIMQDYNYPVEWQSKNPFH---LDDCCVTELSVHRRNNRQTMEDL 304
Db 290 SKRGTLQIMKDRW---NVGHEDDELKPYVEPLDYKDPRTTELWVSMGYTREBIQDS 345

Qy 305 ISLMQYDHLTATYLLLLAKKA--RGKPVRL--RLSSFSCGQASATPPTDIKSNWLSLEV 360
Db 346 LVGQRYNEVMATYLLLYGKSSLEGGDTITLKPRPSADLTNSSAPSPSHKVQ-----RSV 399

Qy 361 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
Db 400 SANPKQR-----RPSDQAGPAIPTSNYSYKK-TOSNNAENK--RPEEDRESGRKA 446

Qy 421 KKNENVYTPKSAVKNEEYFMFPPEKTPVNKNQHKREILTPN-----RYTTPSKARNQC 474
Db 447 SSTAKV-----PASPLPGLERKK---TTPTSTNSVLSTSTNSRNSP 486

Qy 475 LKE-----TPIKIPVNSTGTDKLMGTGVISPER-----R 502
Db 487 LLERASLQOASIQNGKDSAPQRPVVASPSAHNIISSGGAPDRTNPPRGVSSRSTPHAGQ 546

Qy 503 CRSVELDLNQAHEETPK-----RKGA--KVFGS-----LERGL-----DKVITVL 541
Db 547 LRQVR-DQONLPYGVTPASPSSGHSQRRGASGSIFSFTSKFVRRNLNPEKSDRVETLR 605

Qy 542 T-----RSKRKGSARDG-PRRLKLYNNVTTRLVNPDQLNEIMSILPKKHVDF-VOK 592
Db 606 PHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNEMMRIRKVLNDSQCSSELHE 665

Qy 593 GYTLKQCTQSDFGKVTMQFLEVCQIQKPDVVGIRQRLLKGDWAVYKRLVEDILSSCKV 651
Db 666 KYMLLCMHGTGPHGDFVQWEMEVCVCKLRLSLNGVRFKRIISGTSMAFKNIASKIANELKL 724
```

RESULT 10
US-10-274-194-2
; Sequence 2, Application US/10274194
; Patent No. 6706511
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001306DIV
; CURRENT APPLICATION NUMBER: US/10/274,194
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-274-194-2

Query Match 22.3%; Score 769.5; DB 2; Length 724;
Best Local Similarity 30.3%; Pred. No. 4.1e-62;
Matches 218; Conservative 124; Mismatches 252; Indels 125; Gaps 24;

```
Qy 11 YELHETIGTGGAFAKVLACHILTGEMVAIKIMDKNTL-GSDLPRIKTEIEALKNLRHQHI 69
Db 53 YRLKKTIGKGNFAKVLARHILTGKEVAVKIIDKTQLNSSLQKLFREVRIMKVLNHPNI 112

Qy 70 COLYHLETANKIFMWLEYPGCGELFDYIISQDRLSEETRVVFRQIVSAVAVVHSGYA 129
Db 113 VKLFEVETETKLYLVMEYASGEVFDYLVAGHMKKEARAKFRQVVSAYVQYCHQKFIV 172

Qy 130 HRDLKPENLLFDYHKLKLIIDFGLCAK-PKGNKYHLQTCGSLAYAAPELIQGSYLS 188
Db 173 HRDLKAENLLDADMNKIADFGSNEFTFGNK---LDTFCGSPPYAAPELFGQKYDGP 229

Qy 189 EADVMSGILLVLMCGFLPFDDNNMALKYKIMRGKYDVPKWLSPSSILLQOQLQVDP 248
Db 230 EVDVMSGLVLYLVSGSLFPDQNLKELREVRVLRGKRIIPFYMTSDCNLKKFILIHP 289

Qy 249 KKRISMKNLNLHPWIMQDYNYPVEWQSKNPFH---LDDCCVTELSVHRRNNRQTMEDL 304
Db 290 SKRGTLQIMKDRW---NVGHEDDELKPYVEPLDYKDPRTTELWVSMGYTREBIQDS 345

Qy 305 ISLMQYDHLTATYLLLLAKKA--RGKPVRL--RLSSFSCGQASATPPTDIKSNWLSLEV 360
Db 346 LVGQRYNEVMATYLLLYGKSSLEGGDTITLKPRPSADLTNSSAPSPSHKVQ-----RSV 399

Qy 361 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
Db 400 SANPKQR-----RPSDQAGPAIPTSNYSYKK-TOSNNAENK--RPEEDRESGRKA 446

Qy 421 KKNENVYTPKSAVKNEEYFMFPPEKTPVNKNQHKREILTPN-----RYTTPSKARNQC 474
Db 447 SSTAKV-----PASPLPGLERKK---TTPTSTNSVLSTSTNSRNSP 486

Qy 475 LKE-----TPIKIPVNSTGTDKLMGTGVISPER-----R 502
Db 487 LLERASLQOASIQNGKDSAPQRPVVASPSAHNIISSGGAPDRTNPPRGVSSRSTPHAGQ 546

Qy 503 CRSVELDLNQAHEETPK-----RKGA--KVFGS-----LERGL-----DKVITVL 541
Db 547 LRQVR-DQONLPYGVTPASPSSGHSQRRGASGSIFSFTSKFVRRNLNPEKSDRVETLR 605

Qy 542 T-----RSKRKGSARDG-PRRLKLYNNVTTRLVNPDQLNEIMSILPKKHVDF-VOK 592
Db 606 PHVVGSGNDKEKEEFREAKPRSLRFTWSMKTTSMEPNEMMRIRKVLNDSQCSSELHE 665

Qy 593 GYTLKQCTQSDFGKVTMQFLEVCQIQKPDVVGIRQRLLKGDWAVYKRLVEDILSSCKV 651
Db 666 KYMLLCMHGTGPHGDFVQWEMEVCVCKLRLSLNGVRFKRIISGTSMAFKNIASKIANELKL 724
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RESULT 11
US-10-760-407-2
; Sequence 2, Application US/10760407
; Patent No. 6930173
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001306-DIV II
; CURRENT APPLICATION NUMBER: US/10760, 407
; CURRENT FILING DATE: 2004-01-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-760-407-2

Query Match      22.3%; Score 769.5; DB 2; Length 724;
Best Local Similarity 30.3%; Pred. No. 4.1e-62;
Matches 218; Conservative 124; Mismatches 252; Indels 125; Gaps 24;

QY 11 YELHETIGTGPAKVKLACHILTGEMVAIKIMDKNTL-GSDLPRIKTEIALKNLRHQHI 69
DB 53 YRLKTIKGNFAKVKLARHILTGKEVAVKIIDKTLNSSLQKLPREVIMKVLNHPNI 112
QY 70 COLYHVLETANKIFMWLEYCPGELPDYIISQRLSEETRVVFRQIVSAVAVHSGYA 129
DB 113 VKLFEVIEETKTYLVMEYASGGEVDYLVAGHGMKEKEARAKFRQIVSAVOYCHOKFIV 172
QY 130 HRDLKPNLDFDEYHKLKIDFGLCAK-PKGNKDYHLQTCGSLAFAAPELIQGKSYLGS 188
DB 173 HRDLKAENLLDDAMNIIADFGSNEFTFGNK---LDTFCGSPPYAAPLFOGKYDGP 229
QY 189 EADVMSGILLYVLMCGFLPDDDDNMALYKIMRGKYDVPKWLSPSSIIILLQOQLQVDP 248
DB 230 EVDVMSGLVILYLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKFLILNP 289
QY 249 KKRISKNLNLHPWIMQDYNYPVWQSKNPFIIH---LDDCVTELSEVHHRNNRQTMEDL 304
DB 290 SKRGTLLEQIMKDRWM---NVGHEDDELKPYVEPLDYKDPRTTELMSVSMGYTREBIQDS 345
QY 305 ISLWQYDHLTATYLLLLAKKA--RGPVRL--RLSSFCSCQASATPTDIIKSNWMSLEDV 360
DB 346 LVQQRNEVMATYLLLYGKSSLEGGDTITLKPRPSADLTNSSAPSPSHKVVQ-----RSV 399
QY 361 TASDKNVVAGLIDYDMCEDDLSTGAATPRTSOFTKYWTESSNGVESKSLTPALCRTPANKL 420
DB 400 SANPKQR-----RPSDAQGPAIPTSNYSYKK-TQSNNAENK--REEDRESGRKA 446
QY 421 KKNENYTPKSAVNEEYFMFPKPTPVNKNQKHREILTPN-----RYTPPSKARNQC 474
DB 447 SSTAKV-----PASPLGLERKK---TTPSTNSVLSTSTNRSRNSP 486
QY 475 LKE-----TPIKIPVNSTGDKLMTGVISPER-----R 502
DB 487 LLERASLGQASIONGDKSTAPQVAPVSPSAHNISGGGAPDRTNPRGVSSRSTFHAGQ 546
QY 503 CRSVELDLNQAHEETPK-----RKGA--KVFGS-----LBERGL-----DKVITVL 541
DB 547 LRQVR-DQONLPYGVTPASPSGHSQGRGAGSGISFKFTSKFYVRNLNPESEKORVETLR 605
QY 542 T-----RSKRGSGARDG--PRRLKLVNVTTLNPNQOLNEMSIILPKGHVDF-VOK 592
DB 606 PHVVGSGGNDKEKEBEFREAKPRSLREFTWSMKTTSMEPNEMREIRKVLVDANSQCSLHE 665
QY 593 GYTLKCTQSDFGKVTWQRELEVQLQKPDVVGIRERQLKGDWAVYKRLVEDILSSCKV 651
DB 666 KYMLLCMHGTGPHGDFVQWEMEVCKLPRUSLNGVRPKRISGTSMAFKNIASKIANELKL 724
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RESULT 12
US-09-523-849-36
; Sequence 36, Application US/09523849
; Patent No. 6458561
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Molteni, Angela
; APPLICANT: Magnaghi, Paola
; APPLICANT: Bosotti, Roberta
; APPLICANT: Scaccheri, Emanuela
; APPLICANT: Isaccheri, Antonella
; APPLICANT: Hodgson, Dave
; TITLE OF INVENTION: HUMAN NIM1 KINASE
; FILE REFERENCE: PC-0009 US
; CURRENT APPLICATION NUMBER: US/09/523, 849
; CURRENT FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PERL Program
; SEQ ID NO 36
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank Accession No. 6458561 g1749794
US-09-523-849-36

Query Match      22.2%; Score 764.5; DB 2; Length 745;
Best Local Similarity 29.6%; Pred. No. 1.3e-61;
Matches 220; Conservative 136; Mismatches 267; Indels 121; Gaps 27;

QY 11 YELHETIGTGPAKVKLACHILTGEMVAIKIMDKNTL-GSDLPRIKTEIALKNLRHQHI 69
DB 20 YRLKTIKGNFAKVKLARHILTGKEVAVKIIDKTLNSSLQKLPREVIMKVLNHPNI 79
QY 70 COLYHVLETANKIFMWLEYCPGELPDYIISQRLSEETRVVFRQIVSAVAVHSGYA 129
DB 80 VKLFEVIEETKTYLVMEYASGGEVDYLVAGHGMKEKEARAKFRQIVSAVOYCHOKFIV 139
QY 130 HRDLKPNLDFDEYHKLKIDFGLCAK-PKGNKDYHLQTCGSLAFAAPELIQGKSYLGS 188
DB 140 HRDLKAENLLDDAMNIIADFGSNEFTFGNK---LDTFCGSPPYAAPLFOGKYDGP 196
QY 189 EADVMSGILLYVLMCGFLPDDDDNMALYKIMRGKYDVPKWLSPSSIIILLQOQLQVDP 248
DB 197 EVDVMSGLVILYLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKFLILNP 256
QY 249 KKRISKNLNLHPWIMQDYNYPVWQSKNPFIIH---LDDCVTELSEVHHRNNRQTMEDL 304
DB 257 SKRGTLLEQIMKDRWM---NVGHEDDELKPYVEPLDYKDPRTTELMSVSMGYTREBIQDS 312
QY 305 ISLWQYDHLTATYLLLLAKKA--RGPVRL--LSSFCSCQASATP---QASATP---346
DB 313 LVQQRNEVMATYLLLYGKSSLEGGDTITLKPRPSADLTNSSAPSPSHKVVQSVSANPKQ 372
QY 347 --FTD-----IKSNWMSLEDVTSADKNVAVAGLIDYDMCEDDLSTGAATPRTSOFTKYWT 398
DB 373 RRFSDAQGPAIPTSNYSYKKTOSNNAENKRP-----EEDRESGRKASSTAKVPA--S 422
QY 399 EBSNGVESKSLTP-----ALCRTPANKLKNK---ENVYTPKSAVKQ--EYFMFPEPK 445
DB 423 PUPGLERKKTTPPTSTNSVLSTSTNRSRNSPLLERASLGQASIQNGKDSLTPGSRASTA 482
QY 446 -----TPVNKNQKHREILTT--PNRYTPPSKARNQC-----LKETPIKIPVNSTGDKUM 493
DB 483 SASAAVSAARPRQHOKMSMSASVHPKASGLPPTESNCEVPRESTAPQRPVPAASAHNIS 542
QY 494 TGVISPER-----RCRSVELDLNQAHEETPK-----RKGA--KVF 527
DB 543 SSGGAPDRTNPRGVSSRSTFHAGQLRQVR-DQONLPYGVTPASPSGHSQGRGAGSGISF 601
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QY 471 RNQCLKE-----TPIKIPVNSTGTDKLMGTGVISSPER----- 501
Db 481 RNSPLDRLASLGQASIQNGKSDTAPQRPVWASPSPSAHNISSSSGAPDRTNFPRGVSSRSTF 540
QY 502 ---RCSRVELDLNQAHEETPK-----RKGA--KVFGS-----LERGL-----DKV 537
Db 541 HAQQLRQVR--DQONLPGVTVPASPGHSGOGRGASGIFSKFTSKFVRRNLNPEPKDRV 599
QY 538 ITVLTR-----SKRKGARDG--PRLKLNHYNTTTLVNPOLLNEIMSILPKKHVDF 589
Db 600 ETLRPHVVGGGTDKEKEEFREAKPRSLRFTWSMKTTSSMEPNEMREIRKVLDA NSCQS 659
QY 590 -VQGYTLKQOTSDFGKVTMQPELEVCOLOKPDVVGIRQRQLKGDWVYKRLVEDILSS 648
Db 660 ELHERYMLLCVHGTGPHENFVQWEMEVCVKLPRLSLNGVRFKRIISGTSMAFKNIASKIANE 719
QY 649 CKV 651
Db 720 LKL 722

RESULT 15
US-10-760-407-4
; Sequence 4, Application US/10760407
; Patent No. 6930173
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001308-DIV II
; CURRENT APPLICATION NUMBER: US/10/760,407
; CURRENT FILING DATE: 2004-01-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-760-407-4
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Query Match 22.0%; Score 759.5; DB 2; Length 722;
Best Local Similarity 29.7%; Pred. No. 3.5e-61;
Matches 215; Conservative 125; Mismatches 248; Indels 135; Gaps 23;

QY 11 YELHETIGTGPAKVKLACHILTGEMVAIKIMDKNTL-GSDLPRIKTEIEALKNLRHQHI 69
Db 53 YRLKTIKGKFAKVKLARIHLITGKEVAVKIIDKTQLNSSSLQKLPREVIMKVLNHPNI 112
QY 70 CQLYHLETANKIFMVLVPCGGELEFDYIIISQDLSEETRVVFRQIVSAVAYVHSQGYA 129
Db 113 VKLFEVIEETKTLVLMVEYASGGEVFDYLVHGRMKEKEARAKFRQIVSAVQYCHQKFIV 172
QY 130 HRDLKPNILLFDYHKLKLDIFGLCAK-PKGNKDYHLQTCGSLAYAAPELIQKSYLGS 188
Db 173 HRDLKAENLLDADNMKIDAFGFSNEFTGNK---LDTFGSPPYAAPELFQKKYDGP 229
QY 189 EADVWSMGILLYVMCGFLPPDDNNVVALYKIMRGKYDVPKWLSPSSILLQOMLQVDP 248
Db 230 EVDVNSGLVILYLVGSLPFDGQNLKELRERVLRKYRIPPFYMTDCENLLKKFLILNP 289
QY 249 KKRISMKNLNLHPWIMQDYNYPVWOSKNPFIH-----LDDDCVTELSVHRRNNRQTMEDL 304
Db 290 SKRGTLQEQIMKDRW---NVGHEDDELKPYVEPLPDYKDPRTTELWMSMGYTRBEEIQDS 345
QY 305 ISLWQDHLTATYLLALLAKA--RGKPVRL--RLSFSQCGASATPTDIKSNWSLEDV 360
Db 346 LVQRYNEVMATYLLLYGYSSELEGDTITLKPRPSADLTNSSAPSPSHKVQ-----RSV 399
QY 361 TASDKNVVAGLIDYDNCEDDLSTGAATPRTSQFTKYWTESNGVESK-----SLTP 410
Db 400 SANPKOR-----RSSDQAVPAIPTSNYSYK--TQSNNAENKRPEETGRKASSTA 448
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Search completed: November 21, 2006, 14:15:15
Job time: 56 secs

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OM protein - protein search, using sw model

Run on: November 21, 2006, 14:14:30 ; Search time 188 Seconds
(without alignments)
1604.005 Million cell updates/sec

Title: US-10-656-598-2

Perfect score: 3447

Sequence: 1 MKDYDELLKYYELHETIGT.....KGDWVYKRLVEDILSSCKV 651

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC Celerra_SID33/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC Celerra_SID33/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC Celerra_SID33/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC Celerra_SID33/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC Celerra_SID33/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC Celerra_SID33/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3447	100.0	651	3	US-09-870-937-10
2	3447	100.0	651	3	US-09-870-937-10
3	3447	100.0	651	3	US-09-870-937-10
4	3447	100.0	651	4	US-10-354-358-8
5	3447	100.0	651	4	US-10-295-027-506
6	3447	100.0	651	4	US-10-173-999-127
7	3447	100.0	651	5	US-10-656-598-2
8	3447	100.0	651	5	US-10-723-860-2444
9	3447	100.0	651	5	US-10-756-149-5359
10	3447	100.0	651	5	US-10-770-726-67
11	3447	100.0	656	4	US-10-177-138-10
12	3447	100.0	656	4	US-10-425-114-54260
13	3447	100.0	656	4	US-10-425-114-54261
14	1220	35.4	231	3	US-09-764-875-906
15	1176	34.1	272	4	US-10-106-698-5313
16	1156	33.5	726	4	US-10-369-493-5945
17	880	25.5	201	4	US-10-106-698-6277
18	791.5	23.0	713	5	US-10-995-561-881
19	791	22.9	744	3	US-09-835-081-4
20	789.5	22.9	667	4	US-10-016-248-74
21	789.5	22.9	713	4	US-10-161-565-27
22	789.5	22.9	729	5	US-10-995-561-878
23	788.5	22.9	729	4	US-10-142-356-11
24	788.5	22.9	729	4	US-10-195-101-33
25	788.5	22.9	729	4	US-10-161-565-26
26	788	22.9	744	3	US-09-319-585-3
27	788	22.9	744	5	US-10-995-561-876

28	787.5	22.8	737	5	US-10-995-561-880	Sequence 880, App
29	785.5	22.8	733	5	US-10-995-561-877	Sequence 877, App
30	772.5	22.4	731	5	US-10-491-467-27	Sequence 27, App
31	770.5	22.4	691	3	US-09-919-585-6	Sequence 6, Appl
32	770.5	22.4	724	3	US-09-919-585-9	Sequence 9, Appl
33	769.5	22.3	691	5	US-10-756-149-5263	Sequence 5263, Ap
34	769.5	22.3	724	4	US-10-274-194-2	Sequence 2, Appl
35	769.5	22.3	724	4	US-10-760-407-2	Sequence 2, Appl
36	768	22.3	752	5	US-10-995-561-879	Sequence 879, App
37	764.5	22.2	745	4	US-10-195-101-36	Sequence 36, Appl
38	764.5	22.2	745	4	US-10-161-565-24	Sequence 24, Appl
39	764.5	22.2	745	4	US-10-260-708-79	Sequence 79, Appl
40	764.5	22.2	745	5	US-10-737-450-16	Sequence 16, Appl
41	761	22.1	776	4	US-10-366-288-6	Sequence 6, Appl
42	760	22.0	787	4	US-10-618-941-76	Sequence 76, Appl
43	759.5	22.0	722	4	US-10-274-194-4	Sequence 4, Appl
44	759.5	22.0	722	4	US-10-760-407-4	Sequence 4, Appl
45	759.5	22.0	722	5	US-10-784-004-435	Sequence 435, App

ALIGNMENTS

RESULT 1

US-09-870-937-10
; Sequence 10, Application US/09870937
; Patent No. US20020049180A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Bin
; APPLICANT: Seeley, Todd
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEOPLASTIC DISEASE USING
; FILE REFERENCE: 200130.514/PP-01623.002
; CURRENT APPLICATION NUMBER: US/09/870,937
; CURRENT FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-870-937-10

Query Match 100.0%; Score 3447; DB 3; Length 651;
Best Local Similarity 100.0%; Pred. No. 7.8e-251;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKDYDELLKYYELHETIGTGGFAKVKLACHILTGMVAIKIMDKNTLGSDDLPRKTEIEA	60
DB	1	MKDYDELLKYYELHETIGTGGFAKVKLACHILTGMVAIKIMDKNTLGSDDLPRKTEIEA	60
QY	61	LKNLRHQLCOLYHVLETANKIFMWLEYPGCGELFDYIISQDRLSEETRVVFRQIVSAV	120
DB	61	LKNLRHQLCOLYHVLETANKIFMWLEYPGCGELFDYIISQDRLSEETRVVFRQIVSAV	120
QY	121	AYVHSGYAHRLDKPENLLFDBYHKLKLDLFGLCAPKGNKDYHLQTCGSLAYAAPELI	180
DB	121	AYVHSGYAHRLDKPENLLFDBYHKLKLDLFGLCAPKGNKDYHLQTCGSLAYAAPELI	180
QY	181	QKSYLGSEADYVWSMGILLIYVLMCGFLPDDDDNNVMAIYKIMRGKYDVPKWLSPSSILL	240
DB	181	QKSYLGSEADYVWSMGILLIYVLMCGFLPDDDDNNVMAIYKIMRGKYDVPKWLSPSSILL	240
QY	241	QOMLVDPKRIISMKNLNHPIMODYNYPVWSQKNPFIHLDDDCVTELSVHHRNROT	300
DB	241	QOMLVDPKRIISMKNLNHPIMODYNYPVWSQKNPFIHLDDDCVTELSVHHRNROT	300
QY	301	MEDLISLWQYDHLTATYLLLLAKAKGKPVRLRLSSFCGQASATPFTDIKNNWSLEDV	360
DB	301	MEDLISLWQYDHLTATYLLLLAKAKGKPVRLRLSSFCGQASATPFTDIKNNWSLEDV	360
QY	361	TASDKNYVAGLIDYDWCEDDLSTGAATPRTSFTKYTWTESNGVESKSLTPALCRTPANKL	420

Db 361 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
QY 421 KKNENYVTPKSAVKNBEYFMFPPEKTPVKNKQHKREILTPPNRYTTPSKARNQCLKETPI 480
Db 421 KKNENYVTPKSAVKNBEYFMFPPEKTPVKNKQHKREILTPPNRYTTPSKARNQCLKETPI 480
QY 481 KIPVNSTGDKLMTGTVISPERCRSVELDLNQAAMEETPKRGAKVFGSLERGLDKVITV 540
Db 481 KIPVNSTGDKLMTGTVISPERCRSVELDLNQAAMEETPKRGAKVFGSLERGLDKVITV 540
QY 541 LTRSKRGSGARDGPRRLKHLHYNTTTLVNPDPQLNEIMSILPKKHVDVFKQGYTLKCQT 600
Db 541 LTRSKRGSGARDGPRRLKHLHYNTTTLVNPDPQLNEIMSILPKKHVDVFKQGYTLKCQT 600
QY 601 QSDFGKVTWQFELEVQCOLQKPDVVGIRRQRLKGDWVYKRLVEDILSSCKV 651
Db 601 QSDFGKVTWQFELEVQCOLQKPDVVGIRRQRLKGDWVYKRLVEDILSSCKV 651

RESULT 2
US-09-974-298-112
; Sequence 112, Application US/09974298
; Patent No. US20020156263A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Huei-Mei
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/09/974, 298
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,331
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 112
; TYPE: PRT
; LENGTH: 651
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 256716CD1
US-09-974-298-112

Query Match 100.0%; Score 3447; DB 3; Length 651;
Best Local Similarity 100.0%; Pred. No. 7,8e-251;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDYDELLKYYELHETIGTGGFAKVKLACHILTGEMVAIKIMDKNTLGSGLPRIKTEIEA 60
Db 1 MKDYDELLKYYELHETIGTGGFAKVKLACHILTGEMVAIKIMDKNTLGSGLPRIKTEIEA 60
QY 61 LKNLRHQHICQLYHVLETANKI FMVLEYCPGGELFDYIIISQDRLSBEETRVVFRQIVSAV 120
Db 61 LKNLRHQHICQLYHVLETANKI FMVLEYCPGGELFDYIIISQDRLSBEETRVVFRQIVSAV 120
QY 121 AYVHSQGYAHRDLKPENLFLDEYHKLGLIDFGICAKPKGNKDYLQTCGSLAYAAPELI 180
Db 121 AYVHSQGYAHRDLKPENLFLDEYHKLGLIDFGICAKPKGNKDYLQTCGSLAYAAPELI 180
QY 181 QGKSYLEADVMSGILLYVLMCGFLPFPDDNNMALYKKIMRGKYDVPKWLSPSSILL 240
Db 181 QGKSYLEADVMSGILLYVLMCGFLPFPDDNNMALYKKIMRGKYDVPKWLSPSSILL 240
QY 241 QOMLOVDPKKRISMKNLNHPWIMQDYNYPVEWQSKNPPFHLDDDCVTELSVHHRNRQT 300
Db 241 QOMLOVDPKKRISMKNLNHPWIMQDYNYPVEWQSKNPPFHLDDDCVTELSVHHRNRQT 300
QY 301 MEDLISLWQYDHLTATYVLLLLAKARGKPVRLRLSSPSCGQASATPTDIIKSNWSLEDV 360
Db 301 MEDLISLWQYDHLTATYVLLLLAKARGKPVRLRLSSPSCGQASATPTDIIKSNWSLEDV 360
QY 361 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420

Db 361 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
QY 421 KKNENYVTPKSAVKNBEYFMFPPEKTPVKNKQHKREILTPPNRYTTPSKARNQCLKETPI 480
Db 421 KKNENYVTPKSAVKNBEYFMFPPEKTPVKNKQHKREILTPPNRYTTPSKARNQCLKETPI 480
QY 481 KIPVNSTGDKLMTGTVISPERCRSVELDLNQAAMEETPKRGAKVFGSLERGLDKVITV 540
Db 481 KIPVNSTGDKLMTGTVISPERCRSVELDLNQAAMEETPKRGAKVFGSLERGLDKVITV 540
QY 541 LTRSKRGSGARDGPRRLKHLHYNTTTLVNPDPQLNEIMSILPKKHVDVFKQGYTLKCQT 600
Db 541 LTRSKRGSGARDGPRRLKHLHYNTTTLVNPDPQLNEIMSILPKKHVDVFKQGYTLKCQT 600
QY 601 QSDFGKVTWQFELEVQCOLQKPDVVGIRRQRLKGDWVYKRLVEDILSSCKV 651
Db 601 QSDFGKVTWQFELEVQCOLQKPDVVGIRRQRLKGDWVYKRLVEDILSSCKV 651

RESULT 3
US-10-354-358-8
; Sequence 8, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Lesoon, Andrea
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; TITLE OF INVENTION: 7181, 7650, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
; TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
; FILE REFERENCE: MPI02-020PIRNONMIM
; CURRENT APPLICATION NUMBER: US/10/354,358
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/353,600
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/364,517
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/371,075
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/371,507
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 60/372,984
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/374,194
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/382,995
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/385,023
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/388,853
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/389,395
; PRIOR FILING DATE: 2002-06-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-354-358-8

Query Match 100.0%; Score 3447; DB 4; Length 651;


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Best Local Similarity 100.0%; Pred. No. 7.8e-251;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKDYDELLKYELHETIGTGFAKVKLACHILTGEMVAIKIMDKNTLGSDLPRIKTEIEA 60
Db 1 MKDYDELLKYELHETIGTGFAKVKLACHILTGEMVAIKIMDKNTLGSDLPRIKTEIEA 60
Qy 61 LKXLRHQHICOLYHVLETKANKIFMWLEVCYGGELFDYIISQDRLSEETRVVFRQIVSAV 120
Db 61 LKXLRHQHICOLYHVLETKANKIFMWLEVCYGGELFDYIISQDRLSEETRVVFRQIVSAV 120
Qy 121 AYVHSGQYAHARDLKPENLLFDEYHKLLIDFGLCAKPKGNKDYLQTCGSLAYAAPELI 180
Db 121 AYVHSGQYAHARDLKPENLLFDEYHKLLIDFGLCAKPKGNKDYLQTCGSLAYAAPELI 180
Qy 181 QGKSYLGSEADVMSGILLYVLMCGFLPFDDDDNMALYKKIMRGKYDVPKWLSPSSILL 240
Db 181 QGKSYLGSEADVMSGILLYVLMCGFLPFDDDDNMALYKKIMRGKYDVPKWLSPSSILL 240
Qy 241 QOMLQVDPKCRISMKNLNHPIMQDYNYPVSEWQSKNPFILHDDDCVTELSVHHRNROT 300
Db 241 QOMLQVDPKCRISMKNLNHPIMQDYNYPVSEWQSKNPFILHDDDCVTELSVHHRNROT 300
Qy 301 MEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSSFCGQASATPTTDIKNNWSLEDV 360
Db 301 MEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSSFCGQASATPTTDIKNNWSLEDV 360
Qy 361 TASDKNYVAGLIDYDWCEDDLSGTGAATPRTSQTKYWTESNGVESKSLTPALCRTPANKL 420
Db 361 TASDKNYVAGLIDYDWCEDDLSGTGAATPRTSQTKYWTESNGVESKSLTPALCRTPANKL 420
Qy 421 KKNENYVTPKSAVKNEEYFMPPEKTPVNKQHKREILITPNRYTTPSKARNQCLKETPI 480
Db 421 KKNENYVTPKSAVKNEEYFMPPEKTPVNKQHKREILITPNRYTTPSKARNQCLKETPI 480
Qy 481 KIPVNSTGDKLMTGVI SPERRCRSVELDLNQAHMEETPKRGAKVFGSLERGLDKVITV 540
Db 481 KIPVNSTGDKLMTGVI SPERRCRSVELDLNQAHMEETPKRGAKVFGSLERGLDKVITV 540
Qy 541 LTRSRKGSARDGPRRLKHLHYNTTTLVNDPOLLNEIMSLIPKXHVDFVQKGYTLKCO 600
Db 541 LTRSRKGSARDGPRRLKHLHYNTTTLVNDPOLLNEIMSLIPKXHVDFVQKGYTLKCO 600
Qy 601 QSDFGKVTMQFELEVQOLQKPDVVGIRRLKGDAMVYKRLVEDILSSCKV 651
Db 601 QSDFGKVTMQFELEVQOLQKPDVVGIRRLKGDAMVYKRLVEDILSSCKV 651

RESULT 4
US-10-295-027-506
; Sequence 506, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Nataasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Heverzi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500S
; CURRENT FILING DATE: 2002-11-13
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2000-09-15
; PRIOR FILING DATE: 2000-09-15
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR APPLICATION NUMBER: US 60/335,394
```

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Query Match 100.0%; Score 3447; DB 4; Length 651;
Best Local Similarity 100.0%; Pred. No. 7.8e-251;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKDYDELLKYELHETIGTGFAKVKLACHILTGEMVAIKIMDKNTLGSDLPRIKTEIEA 60
Db 1 MKDYDELLKYELHETIGTGFAKVKLACHILTGEMVAIKIMDKNTLGSDLPRIKTEIEA 60
Qy 61 LKXLRHQHICOLYHVLETKANKIFMWLEVCYGGELFDYIISQDRLSEETRVVFRQIVSAV 120
Db 61 LKXLRHQHICOLYHVLETKANKIFMWLEVCYGGELFDYIISQDRLSEETRVVFRQIVSAV 120
Qy 121 AYVHSGQYAHARDLKPENLLFDEYHKLLIDFGLCAKPKGNKDYLQTCGSLAYAAPELI 180
Db 121 AYVHSGQYAHARDLKPENLLFDEYHKLLIDFGLCAKPKGNKDYLQTCGSLAYAAPELI 180
Qy 181 QGKSYLGSEADVMSGILLYVLMCGFLPFDDDDNMALYKKIMRGKYDVPKWLSPSSILL 240
Db 181 QGKSYLGSEADVMSGILLYVLMCGFLPFDDDDNMALYKKIMRGKYDVPKWLSPSSILL 240
Qy 241 QOMLQVDPKCRISMKNLNHPIMQDYNYPVSEWQSKNPFILHDDDCVTELSVHHRNROT 300
Db 241 QOMLQVDPKCRISMKNLNHPIMQDYNYPVSEWQSKNPFILHDDDCVTELSVHHRNROT 300
Qy 301 MEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSSFCGQASATPTTDIKNNWSLEDV 360
Db 301 MEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSSFCGQASATPTTDIKNNWSLEDV 360
Qy 361 TASDKNYVAGLIDYDWCEDDLSGTGAATPRTSQTKYWTESNGVESKSLTPALCRTPANKL 420
Db 361 TASDKNYVAGLIDYDWCEDDLSGTGAATPRTSQTKYWTESNGVESKSLTPALCRTPANKL 420
Qy 421 KKNENYVTPKSAVKNEEYFMPPEKTPVNKQHKREILITPNRYTTPSKARNQCLKETPI 480
Db 421 KKNENYVTPKSAVKNEEYFMPPEKTPVNKQHKREILITPNRYTTPSKARNQCLKETPI 480
Qy 481 KIPVNSTGDKLMTGVI SPERRCRSVELDLNQAHMEETPKRGAKVFGSLERGLDKVITV 540
Db 481 KIPVNSTGDKLMTGVI SPERRCRSVELDLNQAHMEETPKRGAKVFGSLERGLDKVITV 540
Qy 541 LTRSRKGSARDGPRRLKHLHYNTTTLVNDPOLLNEIMSLIPKXHVDFVQKGYTLKCO 600
Db 541 LTRSRKGSARDGPRRLKHLHYNTTTLVNDPOLLNEIMSLIPKXHVDFVQKGYTLKCO 600
Qy 601 QSDFGKVTMQFELEVQOLQKPDVVGIRRLKGDAMVYKRLVEDILSSCKV 651
Db 601 QSDFGKVTMQFELEVQOLQKPDVVGIRRLKGDAMVYKRLVEDILSSCKV 651
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RESULT 5
US-10-173-999-127
; Sequence 127, Application US/10173999
; Publication No. US20040005563A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002420US
; CURRENT APPLICATION NUMBER: US/10/173,999
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/299,234
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/315,287
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 127
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-173-999-127

Query Match 100.0%; Score 3447; DB 4; Length 651;
Best Local Similarity 100.0%; Pred. No. 7.8e-251;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKDYDELLKYYELHETIGTGGAFAKVLACHILTGEMVAIKIMDKNTLGSGLPRIKTEISA 60
Db 1 MKDYDELLKYYELHETIGTGGAFAKVLACHILTGEMVAIKIMDKNTLGSGLPRIKTEISA 60

Qy 61 LKNLRHQHICOLYHVLETANKIFMWLEYCPGGELFDYIIISODRLSEETRVVFRQIVSAV 120
Db 61 LKNLRHQHICOLYHVLETANKIFMWLEYCPGGELFDYIIISODRLSEETRVVFRQIVSAV 120

Qy 121 AYVHSGQYAHARDLKPENLLFDEYHKLKIDFGLCAKPGKNDYHLQTCGSLAYAAPELI 180
Db 121 AYVHSGQYAHARDLKPENLLFDEYHKLKIDFGLCAKPGKNDYHLQTCGSLAYAAPELI 180

Qy 181 QGKSYLGSEADVMSGILLYVLMCGFLPFDDNNMALYKKIMRGKYDVPKWLSPSSILL 240
Db 181 QGKSYLGSEADVMSGILLYVLMCGFLPFDDNNMALYKKIMRGKYDVPKWLSPSSILL 240

Qy 241 QQMLQVDPKKRI SMKNLLNHPWIMQDYNYPVWQSKNPF IHLDDDCVTLSVHHRNNROT 300
Db 241 QQMLQVDPKKRI SMKNLLNHPWIMQDYNYPVWQSKNPF IHLDDDCVTLSVHHRNNROT 300

Qy 301 MEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSFSFCQASATPFTDI KSNNWSLEDV 360
Db 301 MEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSFSFCQASATPFTDI KSNNWSLEDV 360

Qy 361 TASDKNRYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTL PANKL 420
Db 361 TASDKNRYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTL PANKL 420

Qy 421 KKNENYVTPKSAVKNBEYFMFPPEKTPVNKNQHKREILTPNRYTTPSKARNQCLKETPI 480
Db 421 KKNENYVTPKSAVKNBEYFMFPPEKTPVNKNQHKREILTPNRYTTPSKARNQCLKETPI 480

Qy 481 KIPVNSTGTDKLMTGVI SPERRCRSVELDLNQAHEETPKRGAKVFGSLERGLDKVITV 540
Db 481 KIPVNSTGTDKLMTGVI SPERRCRSVELDLNQAHEETPKRGAKVFGSLERGLDKVITV 540

Qy 541 LTRSKRKSARDGPRRLKLYHNVTTLRLVNPDLQLLNEIMSLPKGHVDFVQKGYTLKCCQT 600
Db 541 LTRSKRKSARDGPRRLKLYHNVTTLRLVNPDLQLLNEIMSLPKGHVDFVQKGYTLKCCQT 600

Qy 601 QSDFGKVTMQPELEYCQLQKPDVVGIRQRQLKGDAAWYKRLVEDILSSCKV 651
Db 601 QSDFGKVTMQPELEYCQLQKPDVVGIRQRQLKGDAAWYKRLVEDILSSCKV 651

RESULT 6
US-10-656-598-2
; Sequence 2, Application US/10656598
; Publication No. US20040229232A1
; GENERAL INFORMATION:
; APPLICANT: DAVID P. DAVIS
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: WILLIAM I. WOOD
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P1981RIP1-US
; CURRENT APPLICATION NUMBER: US/10/656,598
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: US 60/410,166
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 2
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-656-598-2

Query Match 100.0%; Score 3447; DB 5; Length 651;
Best Local Similarity 100.0%; Pred. No. 7.8e-251;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKDYDELLKYYELHETIGTGGAFAKVLACHILTGEMVAIKIMDKNTLGSGLPRIKTEISA 60
Db 1 MKDYDELLKYYELHETIGTGGAFAKVLACHILTGEMVAIKIMDKNTLGSGLPRIKTEISA 60

Qy 61 LKNLRHQHICOLYHVLETANKIFMWLEYCPGGELFDYIIISODRLSEETRVVFRQIVSAV 120
Db 61 LKNLRHQHICOLYHVLETANKIFMWLEYCPGGELFDYIIISODRLSEETRVVFRQIVSAV 120

Qy 121 AYVHSGQYAHARDLKPENLLFDEYHKLKIDFGLCAKPGKNDYHLQTCGSLAYAAPELI 180
Db 121 AYVHSGQYAHARDLKPENLLFDEYHKLKIDFGLCAKPGKNDYHLQTCGSLAYAAPELI 180

Qy 181 QGKSYLGSEADVMSGILLYVLMCGFLPFDDNNMALYKKIMRGKYDVPKWLSPSSILL 240
Db 181 QGKSYLGSEADVMSGILLYVLMCGFLPFDDNNMALYKKIMRGKYDVPKWLSPSSILL 240

Qy 241 QQMLQVDPKKRI SMKNLLNHPWIMQDYNYPVWQSKNPF IHLDDDCVTLSVHHRNNROT 300
Db 241 QQMLQVDPKKRI SMKNLLNHPWIMQDYNYPVWQSKNPF IHLDDDCVTLSVHHRNNROT 300

Qy 301 MEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSFSFCQASATPFTDI KSNNWSLEDV 360
Db 301 MEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSFSFCQASATPFTDI KSNNWSLEDV 360

Qy 361 TASDKNRYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTL PANKL 420
Db 361 TASDKNRYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTL PANKL 420

Qy 421 KKNENYVTPKSAVKNBEYFMFPPEKTPVNKNQHKREILTPNRYTTPSKARNQCLKETPI 480
Db 421 KKNENYVTPKSAVKNBEYFMFPPEKTPVNKNQHKREILTPNRYTTPSKARNQCLKETPI 480

Qy 481 KIPVNSTGTDKLMTGVI SPERRCRSVELDLNQAHEETPKRGAKVFGSLERGLDKVITV 540
Db 481 KIPVNSTGTDKLMTGVI SPERRCRSVELDLNQAHEETPKRGAKVFGSLERGLDKVITV 540

Qy 541 LTRSKRKSARDGPRRLKLYHNVTTLRLVNPDLQLLNEIMSLPKGHVDFVQKGYTLKCCQT 600
Db 541 LTRSKRKSARDGPRRLKLYHNVTTLRLVNPDLQLLNEIMSLPKGHVDFVQKGYTLKCCQT 600

QY 601 QSDFGKVTMQFELEVCOQKPDVVGIRRQRLKGDWVYKRLVEDILSSCKV 651
DB 601 QSDFGKVTMQFELEVCOQKPDVVGIRRQRLKGDWVYKRLVEDILSSCKV 651

RESULT 7

US-10-723-860-2444
; Sequence 2444, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05892.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2444
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-2444

Query Match 100.0%; Score 3447; DB 5; Length 651;
Best Local Similarity 100.0%; Pred. No. 7.8e-251; Indels 0; Gaps 0;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDYDELLKYYELHETIGTGGAFAKVLACHILTGEMVAIKMDKNTLGSGLDLPRIKTEIEA 60
DB 1 MKDYDELLKYYELHETIGTGGAFAKVLACHILTGEMVAIKMDKNTLGSGLDLPRIKTEIEA 60

QY 61 LKNLRHQHICQLYHVLETANKIPMWLEYCPGGELFDYIIISQRLSEETRVVFRQIVSAV 120
DB 61 LKNLRHQHICQLYHVLETANKIPMWLEYCPGGELFDYIIISQRLSEETRVVFRQIVSAV 120

QY 121 AYVHSGYGAHRDLKPNLLFDEYHKLLIDFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180
DB 121 AYVHSGYGAHRDLKPNLLFDEYHKLLIDFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180

QY 181 QGKSYLGSEADVWSMGILLVLMCGFLPDDDDNNVALYKKIMRGKYDVPKWLSPSSILL 240
DB 181 QGKSYLGSEADVWSMGILLVLMCGFLPDDDDNNVALYKKIMRGKYDVPKWLSPSSILL 240

QY 241 QQMLQVDPKKRISMKNLLNHPIMQDYNYPVEWQSKNPFHLLDDCCVTLSVHHRNROT 300
DB 241 QQMLQVDPKKRISMKNLLNHPIMQDYNYPVEWQSKNPFHLLDDCCVTLSVHHRNROT 300

QY 301 MEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSSFCGQASATPFTDIKNNWSLEDV 360
DB 301 MEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSSFCGQASATPFTDIKNNWSLEDV 360

QY 361 TASDKNYVAGLIDYDWCEDDLSGTAAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
DB 361 TASDKNYVAGLIDYDWCEDDLSGTAAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420

QY 421 KKNENYVTPKSAVKNEEYFMPPEKTPVNKNQHKREILTPNRYTTPSKARNQCLKETPI 480
DB 421 KKNENYVTPKSAVKNEEYFMPPEKTPVNKNQHKREILTPNRYTTPSKARNQCLKETPI 480

QY 481 KIPVNSTGDKLMTGVIISPERRCRSVELDLNOAHMEETPKRGAKVFGSLERGLDKVITV 540
DB 481 KIPVNSTGDKLMTGVIISPERRCRSVELDLNOAHMEETPKRGAKVFGSLERGLDKVITV 540

QY 541 LTRSRKRGSGARDGPRRLKHLHYNTTTRLVNPDLQLINEIMSILPKKHVDVFOQGYTLKCO 600
DB 541 LTRSRKRGSGARDGPRRLKHLHYNTTTRLVNPDLQLINEIMSILPKKHVDVFOQGYTLKCO 600

QY 601 QSDFGKVTMQFELEVCOQKPDVVGIRRQRLKGDWVYKRLVEDILSSCKV 651

DB 601 QSDFGKVTMQFELEVCOQKPDVVGIRRQRLKGDWVYKRLVEDILSSCKV 651

RESULT 8

US-10-756-149-5359
; Sequence 5359, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5359
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5359

Query Match 100.0%; Score 3447; DB 5; Length 651;
Best Local Similarity 100.0%; Pred. No. 7.8e-251; Indels 0; Gaps 0;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDYDELLKYYELHETIGTGGAFAKVLACHILTGEMVAIKMDKNTLGSGLDLPRIKTEIEA 60
DB 1 MKDYDELLKYYELHETIGTGGAFAKVLACHILTGEMVAIKMDKNTLGSGLDLPRIKTEIEA 60

QY 61 LKNLRHQHICQLYHVLETANKIPMWLEYCPGGELFDYIIISQRLSEETRVVFRQIVSAV 120
DB 61 LKNLRHQHICQLYHVLETANKIPMWLEYCPGGELFDYIIISQRLSEETRVVFRQIVSAV 120

QY 121 AYVHSGYGAHRDLKPNLLFDEYHKLLIDFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180
DB 121 AYVHSGYGAHRDLKPNLLFDEYHKLLIDFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180

QY 181 QGKSYLGSEADVWSMGILLVLMCGFLPDDDDNNVALYKKIMRGKYDVPKWLSPSSILL 240
DB 181 QGKSYLGSEADVWSMGILLVLMCGFLPDDDDNNVALYKKIMRGKYDVPKWLSPSSILL 240

QY 241 QQMLQVDPKKRISMKNLLNHPIMQDYNYPVEWQSKNPFHLLDDCCVTLSVHHRNROT 300
DB 241 QQMLQVDPKKRISMKNLLNHPIMQDYNYPVEWQSKNPFHLLDDCCVTLSVHHRNROT 300

QY 301 MEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSSFCGQASATPFTDIKNNWSLEDV 360
DB 301 MEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSSFCGQASATPFTDIKNNWSLEDV 360

QY 361 TASDKNYVAGLIDYDWCEDDLSGTAAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
DB 361 TASDKNYVAGLIDYDWCEDDLSGTAAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420

QY 421 KKNENYVTPKSAVKNEEYFMPPEKTPVNKNQHKREILTPNRYTTPSKARNQCLKETPI 480
DB 421 KKNENYVTPKSAVKNEEYFMPPEKTPVNKNQHKREILTPNRYTTPSKARNQCLKETPI 480

QY 481 KIPVNSTGDKLMTGVIISPERRCRSVELDLNOAHMEETPKRGAKVFGSLERGLDKVITV 540
DB 481 KIPVNSTGDKLMTGVIISPERRCRSVELDLNOAHMEETPKRGAKVFGSLERGLDKVITV 540

QY 541 LTRSRKRGSGARDGPRRLKHLHYNTTTRLVNPDLQLINEIMSILPKKHVDVFOQGYTLKCO 600
DB 541 LTRSRKRGSGARDGPRRLKHLHYNTTTRLVNPDLQLINEIMSILPKKHVDVFOQGYTLKCO 600

QY 601 QSDFGKVTMQFELEVCOQKPDVVGIRRQRLKGDWVYKRLVEDILSSCKV 651
DB 601 QSDFGKVTMQFELEVCOQKPDVVGIRRQRLKGDWVYKRLVEDILSSCKV 651

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RESULT 9
US-10-770-726-67
; Sequence 67, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-67

Query Match      100.0%; Score 3447; DB 5; Length 651;
Best Local Similarity 100.0%; Pred. No. 7.8e-251;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDYDELLKYYELHETIGTGPAKVKLACHILTGEMVAIKIMDKNTLGSDDLPRIKTEIEA 60
DB 1 MKDYDELLKYYELHETIGTGPAKVKLACHILTGEMVAIKIMDKNTLGSDDLPRIKTEIEA 60
QY 61 LKNLRHQHICOLYHVLETANKIFMWLEYCPGGELFDYIISQDRLSEETRVVFRQIVSAV 120
DB 61 LKNLRHQHICOLYHVLETANKIFMWLEYCPGGELFDYIISQDRLSEETRVVFRQIVSAV 120
QY 121 AYVHSGQYAHARDLKPENLLFDEYHKLIDFGLCAKPGKNDYHLQTCGSLAYAAPELI 180
DB 121 AYVHSGQYAHARDLKPENLLFDEYHKLIDFGLCAKPGKNDYHLQTCGSLAYAAPELI 180
QY 181 QGKSYLGSEADVWSMGILLVLMCGFLPDDDDNMALYKKIMRGKYDVPKWLSPSSILL 240
DB 181 QGKSYLGSEADVWSMGILLVLMCGFLPDDDDNMALYKKIMRGKYDVPKWLSPSSILL 240
QY 241 QQMLQVDPKKRISMKNLLNHPWIMQDYNYPVEWQSKNPFILHDDDCVTLSVHHRNROT 300
DB 241 QQMLQVDPKKRISMKNLLNHPWIMQDYNYPVEWQSKNPFILHDDDCVTLSVHHRNROT 300
QY 301 MEDLISLWQYDHLTATYLLILLAKKARGKPVRLRLSSFCGQASATPFTDIKSNNWSLEDV 360
DB 301 MEDLISLWQYDHLTATYLLILLAKKARGKPVRLRLSSFCGQASATPFTDIKSNNWSLEDV 360
QY 361 TASDKNYYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
DB 361 TASDKNYYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
QY 421 KKNENYVTPKSAVKNEEYFMFPPEKTPVNKNQHKREILTTPNRYTTPSKARNQCLKETPI 480
DB 421 KKNENYVTPKSAVKNEEYFMFPPEKTPVNKNQHKREILTTPNRYTTPSKARNQCLKETPI 480
QY 481 KIPVNSTGTDKMTGVIISPERRCRSVELDLNOAHMEETPKRGAKVFGSLERGLDKVITV 540
DB 481 KIPVNSTGTDKMTGVIISPERRCRSVELDLNOAHMEETPKRGAKVFGSLERGLDKVITV 540
QY 541 LTRSKRGKSARDGPRLKHLHYNTTTRLVNPDOLLNEIMSILPKKHVDVFOQGYTLKCQT 600
DB 541 LTRSKRGKSARDGPRLKHLHYNTTTRLVNPDOLLNEIMSILPKKHVDVFOQGYTLKCQT 600
QY 601 QSDFGKVTMQFLEVCQLOKPDVVGIRORLKGDAWYKRLVEDIILSSCKV 651
DB 601 QSDFGKVTMQFLEVCQLOKPDVVGIRORLKGDAWYKRLVEDIILSSCKV 651
```

RESULT 10
US-11-177-138-10
; Sequence 10, Application US/11177138

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Publication No. US20050282766A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Bin
; APPLICANT: Seeley, Todd
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEOPLASTIC DISEASE USING
; FILE REFERENCE: 200130.514/PP-01623.002
; CURRENT APPLICATION NUMBER: US/11/177,138
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: US/09/870,937
; PRIOR FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-177-138-10

Query Match      100.0%; Score 3447; DB 6; Length 651;
Best Local Similarity 100.0%; Pred. No. 7.8e-251;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDYDELLKYYELHETIGTGPAKVKLACHILTGEMVAIKIMDKNTLGSDDLPRIKTEIEA 60
DB 1 MKDYDELLKYYELHETIGTGPAKVKLACHILTGEMVAIKIMDKNTLGSDDLPRIKTEIEA 60
QY 61 LKNLRHQHICOLYHVLETANKIFMWLEYCPGGELFDYIISQDRLSEETRVVFRQIVSAV 120
DB 61 LKNLRHQHICOLYHVLETANKIFMWLEYCPGGELFDYIISQDRLSEETRVVFRQIVSAV 120
QY 121 AYVHSGQYAHARDLKPENLLFDEYHKLIDFGLCAKPGKNDYHLQTCGSLAYAAPELI 180
DB 121 AYVHSGQYAHARDLKPENLLFDEYHKLIDFGLCAKPGKNDYHLQTCGSLAYAAPELI 180
QY 181 QGKSYLGSEADVWSMGILLVLMCGFLPDDDDNMALYKKIMRGKYDVPKWLSPSSILL 240
DB 181 QGKSYLGSEADVWSMGILLVLMCGFLPDDDDNMALYKKIMRGKYDVPKWLSPSSILL 240
QY 241 QQMLQVDPKKRISMKNLLNHPWIMQDYNYPVEWQSKNPFILHDDDCVTLSVHHRNROT 300
DB 241 QQMLQVDPKKRISMKNLLNHPWIMQDYNYPVEWQSKNPFILHDDDCVTLSVHHRNROT 300
QY 301 MEDLISLWQYDHLTATYLLILLAKKARGKPVRLRLSSFCGQASATPFTDIKSNNWSLEDV 360
DB 301 MEDLISLWQYDHLTATYLLILLAKKARGKPVRLRLSSFCGQASATPFTDIKSNNWSLEDV 360
QY 361 TASDKNYYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
DB 361 TASDKNYYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
QY 421 KKNENYVTPKSAVKNEEYFMFPPEKTPVNKNQHKREILTTPNRYTTPSKARNQCLKETPI 480
DB 421 KKNENYVTPKSAVKNEEYFMFPPEKTPVNKNQHKREILTTPNRYTTPSKARNQCLKETPI 480
QY 481 KIPVNSTGTDKMTGVIISPERRCRSVELDLNOAHMEETPKRGAKVFGSLERGLDKVITV 540
DB 481 KIPVNSTGTDKMTGVIISPERRCRSVELDLNOAHMEETPKRGAKVFGSLERGLDKVITV 540
QY 541 LTRSKRGKSARDGPRLKHLHYNTTTRLVNPDOLLNEIMSILPKKHVDVFOQGYTLKCQT 600
DB 541 LTRSKRGKSARDGPRLKHLHYNTTTRLVNPDOLLNEIMSILPKKHVDVFOQGYTLKCQT 600
QY 601 QSDFGKVTMQFLEVCQLOKPDVVGIRORLKGDAWYKRLVEDIILSSCKV 651
DB 601 QSDFGKVTMQFLEVCQLOKPDVVGIRORLKGDAWYKRLVEDIILSSCKV 651
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RESULT 11
US-10-425-114-54260
; Sequence 54260, Application US/10425114
; Publication No. US20040034888A1

Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 54260
LENGTH: 656
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Clone ID: LIB4649-035-D9_FLI.pep
US-10-425-114-54260

Query Match 100.0%; Score 3447; DB 4; Length 656;
Best Local Similarity 100.0%; Pred. No. 7.9e-251;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDYDELLKYELHETIGTGGPAKVKLACHILTGEMVAIKIMDKNTLGSGLDLPRIKTEIEA 60
DB 6 MKDYDELLKYELHETIGTGGPAKVKLACHILTGEMVAIKIMDKNTLGSGLDLPRIKTEIEA 65
QY 61 LKNLRHQHICOLYHVLETANKIFWLEYCPGSELFDYIISODRLSEETRVVFRQIVSAV 120
DB 66 LKNLRHQHICOLYHVLETANKIFWLEYCPGSELFDYIISODRLSEETRVVFRQIVSAV 125
QY 121 AYVHSGQYAHRLDKPENLFLFDEYHKLKIDFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180
DB 126 AYVHSGQYAHRLDKPENLFLFDEYHKLKIDFGLCAKPKGNKDYHLQTCGSLAYAAPELI 185
QY 181 QGKSYLGSEADVWSMGILLIYVLMCGFLPFDDNNMALYKKIMRGKYDVPKWLSPSSILL 240
DB 186 QGKSYLGSEADVWSMGILLIYVLMCGFLPFDDNNMALYKKIMRGKYDVPKWLSPSSILL 245
QY 241 QOMLQVDPKKRISMKNLLNHPWIMQDYNYPVWQSKNPFILHDDDCVTELSVHHRNROT 300
DB 246 QOMLQVDPKKRISMKNLLNHPWIMQDYNYPVWQSKNPFILHDDDCVTELSVHHRNROT 305
QY 301 MEDLISLWQYDHLTATYLLILLAKKARGKPVRLRLSSFCQASATPFTDIKSNWNSLEDV 360
DB 306 MEDLISLWQYDHLTATYLLILLAKKARGKPVRLRLSSFCQASATPFTDIKSNWNSLEDV 365
QY 361 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTLPAK 420
DB 366 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTLPAK 425
QY 421 KKNENYTPKSAVKNEEYFMPPEPKTPVNQNHKREILTPNRYTTPSKARNQCLKETPI 480
DB 426 KKNENYTPKSAVKNEEYFMPPEPKTPVNQNHKREILTPNRYTTPSKARNQCLKETPI 485
QY 481 KIPVNSTGTDKLTMTGVI SPERRCRSVELDLNQAHEETPKRGAKVFGSLERGLDKVITV 540
DB 486 KIPVNSTGTDKLTMTGVI SPERRCRSVELDLNQAHEETPKRGAKVFGSLERGLDKVITV 545
QY 541 LTRSKRKSARDGPRRLKHLHYNTTTRLVNPDQLNEIMSILPKGHVDFVQGYTLKCCQT 600
DB 546 LTRSKRKSARDGPRRLKHLHYNTTTRLVNPDQLNEIMSILPKGHVDFVQGYTLKCCQT 605
QY 601 QSDFGKVTMQFELEVCOLOKPDVVGIRRORLKGDAWYKRLVEDILSSCKV 651
DB 606 QSDFGKVTMQFELEVCOLOKPDVVGIRRORLKGDAWYKRLVEDILSSCKV 656

RESULT 12
US-10-425-114-54261
; Sequence 54261, Application US/10425114

Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 54261
LENGTH: 656
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Clone ID: LIB4676-059-GI_FLI.pep
US-10-425-114-54261

Query Match 100.0%; Score 3447; DB 4; Length 656;
Best Local Similarity 100.0%; Pred. No. 7.9e-251;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKDYDELLKYELHETIGTGGPAKVKLACHILTGEMVAIKIMDKNTLGSGLDLPRIKTEIEA 60
DB 6 MKDYDELLKYELHETIGTGGPAKVKLACHILTGEMVAIKIMDKNTLGSGLDLPRIKTEIEA 65
QY 61 LKNLRHQHICOLYHVLETANKIFWLEYCPGSELFDYIISODRLSEETRVVFRQIVSAV 120
DB 66 LKNLRHQHICOLYHVLETANKIFWLEYCPGSELFDYIISODRLSEETRVVFRQIVSAV 125
QY 121 AYVHSGQYAHRLDKPENLFLFDEYHKLKIDFGLCAKPKGNKDYHLQTCGSLAYAAPELI 180
DB 126 AYVHSGQYAHRLDKPENLFLFDEYHKLKIDFGLCAKPKGNKDYHLQTCGSLAYAAPELI 185
QY 181 QGKSYLGSEADVWSMGILLIYVLMCGFLPFDDNNMALYKKIMRGKYDVPKWLSPSSILL 240
DB 186 QGKSYLGSEADVWSMGILLIYVLMCGFLPFDDNNMALYKKIMRGKYDVPKWLSPSSILL 245
QY 241 QOMLQVDPKKRISMKNLLNHPWIMQDYNYPVWQSKNPFILHDDDCVTELSVHHRNROT 300
DB 246 QOMLQVDPKKRISMKNLLNHPWIMQDYNYPVWQSKNPFILHDDDCVTELSVHHRNROT 305
QY 301 MEDLISLWQYDHLTATYLLILLAKKARGKPVRLRLSSFCQASATPFTDIKSNWNSLEDV 360
DB 306 MEDLISLWQYDHLTATYLLILLAKKARGKPVRLRLSSFCQASATPFTDIKSNWNSLEDV 365
QY 361 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTLPAK 420
DB 366 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTLPAK 425
QY 421 KKNENYTPKSAVKNEEYFMPPEPKTPVNQNHKREILTPNRYTTPSKARNQCLKETPI 480
DB 426 KKNENYTPKSAVKNEEYFMPPEPKTPVNQNHKREILTPNRYTTPSKARNQCLKETPI 485
QY 481 KIPVNSTGTDKLTMTGVI SPERRCRSVELDLNQAHEETPKRGAKVFGSLERGLDKVITV 540
DB 486 KIPVNSTGTDKLTMTGVI SPERRCRSVELDLNQAHEETPKRGAKVFGSLERGLDKVITV 545
QY 541 LTRSKRKSARDGPRRLKHLHYNTTTRLVNPDQLNEIMSILPKGHVDFVQGYTLKCCQT 600
DB 546 LTRSKRKSARDGPRRLKHLHYNTTTRLVNPDQLNEIMSILPKGHVDFVQGYTLKCCQT 605
QY 601 QSDFGKVTMQFELEVCOLOKPDVVGIRRORLKGDAWYKRLVEDILSSCKV 651
DB 606 QSDFGKVTMQFELEVCOLOKPDVVGIRRORLKGDAWYKRLVEDILSSCKV 656

RESULT 13
US-10-425-114-54262

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; Sequence 54262, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54262
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4119-174-G9_FLI.pep
US-10-425-114-54262

Query Match      100.0%; Score 3447; DB 4; Length 656;
Best Local Similarity 100.0%; Pred. No. 7.9e-251;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKDYDELLKYYELHETIGTGGAFAKVKLACHILTGEMVAIKIMDKNTLGSDDLPRIKTEISA 60
DB      6 MKDYDELLKYYELHETIGTGGAFAKVKLACHILTGEMVAIKIMDKNTLGSDDLPRIKTEISA 65

QY      61 LKNLRHQHICQLHVLETTANKIFMWLEVCYCGGLFDYIISQRLSBEETRVVFRQIVSAV 120
DB      66 LKNLRHQHICQLHVLETTANKIFMWLEVCYCGGLFDYIISQRLSBEETRVVFRQIVSAV 125

QY      121 AYVHSGQYAHARDLKPENLLFDEYHKLKIDFGICAKPGKNDYHLQTCGSLAYAAPELI 180
DB      126 AYVHSGQYAHARDLKPENLLFDEYHKLKIDFGICAKPGKNDYHLQTCGSLAYAAPELI 185

QY      181 QGKSYLGSEADVWSMGILLVYLMCGFLPDDDDNMALYKKIMRGKYDVPKWLSP 240
DB      186 QGKSYLGSEADVWSMGILLVYLMCGFLPDDDDNMALYKKIMRGKYDVPKWLSP 245

QY      241 QQMLQVDPKKRISMKNLNHPWIMQDYNYPVEWQSNPFIHLDDDCVTBLSVHHRNRQT 300
DB      246 QQMLQVDPKKRISMKNLNHPWIMQDYNYPVEWQSNPFIHLDDDCVTBLSVHHRNRQT 305

QY      301 MEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSFSQASATPFTDIKNNWSLEDV 360
DB      306 MEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSFSQASATPFTDIKNNWSLEDV 365

QY      361 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 420
DB      366 TASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL 425

QY      421 KKNENYVTPKSAVKNREYFMFPBKTPVNKNQHKREILTPNRYTTPSKARNQCLKETPI 480
DB      426 KKNENYVTPKSAVKNREYFMFPBKTPVNKNQHKREILTPNRYTTPSKARNQCLKETPI 485

QY      481 KIPVNSTGTDKLMGTGISPERRCRSVELDLNQAHMEETPKRGAQVFGSLERGLDKVITV 540
DB      486 KIPVNSTGTDKLMGTGISPERRCRSVELDLNQAHMEETPKRGAQVFGSLERGLDKVITV 545

QY      541 LTRSKRGSGARDGPRRLKLNHYNTTTLVNPQDLNEIMSIILPKKHVDVFOKGYYTLKCQT 600
DB      546 LTRSKRGSGARDGPRRLKLNHYNTTTLVNPQDLNEIMSIILPKKHVDVFOKGYYTLKCQT 605

QY      601 QSDFGKVTMQFELEVQOLQKPDVVGIRRRQRLKGDWVYKRLVEDIILSSCKV 651
DB      606 QSDFGKVTMQFELEVQOLQKPDVVGIRRRQRLKGDWVYKRLVEDIILSSCKV 656
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. RESULT 14

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US-09-764-875-906
; Sequence 906, Application US/09764875
; Publication No. US20040018969A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ202
; CURRENT APPLICATION NUMBER: US/09/764,875
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1249
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 906
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (206)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (219)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (234)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (250)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-875-906

Query Match      35.4%; Score 1220; DB 3; Length 251;
Best Local Similarity 98.3%; Pred. No. 1.5e-83;
Matches 230; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 MKDYDELLKYYELHETIGTGGAFAKVKLACHILTGEMVAIKIMDKNTLGSDDLPRIKTEISA 60
DB      6 MKDYDELLKYYELHETIGTGGAFAKVKLACHILTGEMVAIKIMDKNTLGSDDLPRIKTEISA 65

QY      61 LKNLRHQHICQLHVLETTANKIFMWLEVCYCGGLFDYIISQRLSBEETRVVFRQIVSAV 120
DB      66 LKNLRHQHICQLHVLETTANKIFMWLEVCYCGGLFDYIISQRLSBEETRVVFRQIVSAV 125

QY      121 AYVHSGQYAHARDLKPENLLFDEYHKLKIDFGICAKPGKNDYHLQTCGSLAYAAPELI 180
DB      126 AYVHSGQYAHARDLKPENLLFDEYHKLKIDFGICAKPGKNDYHLQTCGSLAYAAPELI 185

QY      181 QGKSYLGSEADVWSMGILLVYLMCGFLPDDDDNMALYKKIMRGKYDVPKWLSP 234
DB      186 QGKSYLGSEADVWSMGILLVYLMCGFLPDDDDNMALYKKIMRGKYDVGKXWLSP 239

RESULT 15
US-10-106-698-5313
; Sequence 5313, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 5313
; LENGTH: 272
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (220)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-5313

Query Match      34.1%; Score 1176; DB 4; Length 272;
Best Local Similarity 84.1%; Pred. No. 3.4e-80;
Matches 227; Conservative 8; Mismatches 35; Indels 0; Gaps 0;

QY 285 DCVTELSVHRRNRQTWEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSSPSCGOASA 344
Db 1 DCVTELSVHRRNRQTWEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSSPSCGOASA 60

QY 345 TPFTDIKSNNWSLEDVTASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVE 404
Db 61 TPFTDIKSNNWSLEDVTASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVE 120

QY 405 SKSLTPALCCTPANKLNKENVTTPKSAVNKEEYFMPEPKTPVNKNQHKREILTTPNRY 464
Db 121 SKSLTPALCCTPANKLNKENVTTPKSAVNKEEYFMPEPKTPVNKNQHKREILTTPNRY 180

QY 465 TTESKARNOCLETPIKIPVNSTGDKLMTGVISPERRCRSVELDLNQAHMEETPKRKGA 524
Db 181 TTESKARNOCLETPIKIPVNSTGDKLMTGVISPERRCRSVELDLNQAHMEETPKRKGA 240

QY 525 KVFGLSLERGLDKVITVLTTRSKRKGSDGP 554
Db 241 KCLGALKGGWIRLSLCSGPAKGRVLPETGP 270
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Search completed: November 21, 2006, 14:18:29
Job time : 190 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: November 21, 2006, 14:15:30 ; Search time 44 Seconds
(without alignments)
1264.753 Million cell updates/sec

Title: US-10-656-598-2
Perfect score: 3447
Sequence: 1 MKDYELLKYYELHETIGT.....KGDWYVKRLVEDILSSCKV 651

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 330775 seqs, 85482512 residues

Total number of hits satisfying chosen parameters: 330775

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New.*

- 1: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 2: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	788.5	22.9	729	US-11-377-316-154	Sequence 154, Appl
2	672	19.5	550	US-11-145-471-1	Sequence 1, Appl
3	672	19.5	550	US-11-145-471-23	Sequence 23, Appl
4	669	19.4	548	US-11-145-471-12	Sequence 12, Appl
5	669	19.4	548	US-11-145-471-18	Sequence 18, Appl
6	648.5	18.8	505	US-10-449-902-45099	Sequence 45099, A
7	647	18.8	461	US-10-449-902-43486	Sequence 43486, A
8	647	18.8	552	US-11-145-471-24	Sequence 24, Appl
9	644	18.7	552	US-11-145-471-36	Sequence 36, Appl
10	644	18.7	552	US-11-145-471-37	Sequence 37, Appl
11	640.5	18.6	509	US-10-449-902-50922	Sequence 50922, A
12	640.5	18.6	509	US-10-449-902-53192	Sequence 53192, A
13	637.5	18.5	545	US-10-449-902-47226	Sequence 47226, A
14	637	18.5	454	US-10-449-902-53399	Sequence 53399, A
15	636.5	18.5	826	US-10-449-902-41270	Sequence 41270, A
16	636.5	18.5	826	US-10-449-902-41270	Sequence 41270, A
17	635	18.4	372	US-10-953-349-10927	Sequence 10927, A
18	633	18.4	454	US-10-449-902-29700	Sequence 29700, A
19	631.5	18.3	494	US-10-449-902-80926	Sequence 80926, A
20	631	18.3	626	US-11-145-471-45	Sequence 45, Appl
21	627	18.2	562	US-11-145-471-35	Sequence 35, Appl
22	627	18.2	624	US-11-145-471-46	Sequence 46, Appl
23	626.5	18.2	422	US-10-953-349-17556	Sequence 17556, A
24	626.5	18.2	794	US-11-320-072-74	Sequence 74, Appl
25	626	18.2	503	US-11-174-307B-4802	Sequence 4802, Ap

ALIGNMENTS

RESULT 1

US-11-377-316-154
; Sequence 154, Application US/11377316
; Publication No. US20060234344A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY D.
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; APPLICANT: SUDERSANAM, SUCHA
; TITLE OF INVENTION: PROTEIN KINASES
; FILE REFERENCE: 038602/1273
; CURRENT APPLICATION NUMBER: US/11/377,316
; CURRENT FILING DATE: 2006-03-17
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 154
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-377-316-154

Query Match	22.9%	Score	788.5	DB	7	Length	729
Best Local Similarity	30.0%	Pred. No.	3.7e-34				
Matches	216	Conservative	124	Mismatches	256	Indels	123
Gaps	20						
QY	11	YELHETIGTGSPAKVKLACHILTGEMVAIKIMDKNTLG-SDLPRIKTEIALKNLRHQHI	69				
Db	56	YRLKTKTGKGNFAKVKLARHILTGREVAIKIIDKTLNPTSLQKLPREVIMKILNHPNI	115				
QY	70	COLYHVEITANKIPWLEVCPCGELFDYIISODRLSEETRVVFRQIVSAVYHSGYA	129				
Db	116	VKLFEVETKTLTYLIMEYASGGEVFDYLVAGRMKEKRSKFRQIVSAVQCHOKRIV	175				
QY	130	HRDLKPNILFDYHKLKILDFGLCAK-PKGNKDVHLOTCCGSLAAYAAPELIQKSYLGS	188				
Db	176	HRDLKAENLLDADNMNIKIDAFGNEFTVGK---LDTFCGSPPPAAELFGKKYDGP	232				
QY	189	EADVMSGILLYVLMCGPLFPDDNNVMALYKKIMRGYDVPKWLSPSSILLQOOLQVDP	248				
Db	233	EVDVMSGLVILTYLVSGSLPFDGQNLKELRERVLGRKYRIPFVMSDTCENLLKRLVLNP	292				
QY	249	KGRISKNLLNHPWIMQDYNYPVWQSKNPFFH----LDDCVTELVSVHRNNRQTMEDL	304				
Db	293	IKRGTLQIMQDRIW-----NAGHEEDLKPFFPELIDISDKRIDIMVGMGYSQEEIQS	348				
QY	305	ISLWQYDHLTATYLLLLAKKARGKPVRLRLSFSQCSQASATPFTDIKSNW-----	355				
Db	349	LSRMKYDEITATY-LLLGKRSSELDASDSSSSNLSLAKVRPSSDLNNSTGSPPHKVOR	407				

Sequence 80197, A
Sequence 48679, A
Sequence 49795, A
Sequence 80196, A
Sequence 80195, A
Sequence 152, App
Sequence 54336, A
Sequence 89481, A
Sequence 93237, A
Sequence 89485, A
Sequence 93241, A
Sequence 47226, A
Sequence 47761, A
Sequence 55509, A
Sequence 6637, Ap
Sequence 35664, A
Sequence 35665, A
Sequence 155, App
Sequence 2, Appli
Sequence 2649, Ap

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QY 356 -----SLEDVTASDKNYVAGLIDYDWCEDDLST----- 383
Db 408 SVSSSQORRYSDHAGPAISVVAYPKBSQTSADGDLKEDGDSRKSAGVGGKIAP 467
QY 384 -----GAATP-----RTSQFTKYWTESNGVSKSLTPALCRTPANKLKNKENVYT 428
Db 468 ASPMLGNASPNKADIPERKSKSTVPSSNTASGWTTRNTYVCSERTTADR----- 518
QY 429 PKSAVN-ERYFPPPKTPVKNQHKREILTTPNRYTTSPKARNQCLKETPIKIPVNST 487
Db 519 -HSVIQNGKNSPTIPQRTV-ASTHSISSAATPDR-----IRFP---R 557
QY 488 GTDKLMTGVISP-ERRC-----RSVELDLNOAHMBETPKRKGAKVFGSLERGLDKVIT 539
Db 558 GTASRSTFHQOPRRTATYNGPPAPSPLSHEATPLSQTSRSGSTNLF-----SKLTS 610
QY 540 VLTRSK-----RKSGARDG-PRRLKLHYNVTTTLVNPQDLNLEIMSLPKKHVDVQK- 592
Db 611 KLTRSNVSAEQDENKEAKPRSLRFTWSMKTTSMDPGDMREIRKVLNANNCDYEORE 670
QY 593 GYTLKCOQTSDFKVTMOPFEVCOLOKQPDVVGIRQRLKGDWVVKLVEDILSSCKV 651
Db 671 RFLLCVHGDAENLVQWEMEVCKPLRLSLNGVRFKRISGTSIAPFKNTASKIANELKL 729

RESULT 2
US-11-145-471-1
; Sequence 1, Application US/11145471
; Publication No. US20060147947A1
; GENERAL INFORMATION:
; APPLICANT: Apfeld, Javier
; APPLICANT: O'Conner, Gregory
; TITLE OF INVENTION: AMPK Pathway Components
; FILE REFERENCE: 13407-0570011
; CURRENT APPLICATION NUMBER: US/11/145,471
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: PCT/US/2003/38628
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/430,804
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: US 60/488,261
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 60/578,804
; PRIOR FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-145-471-1

Query Match 19.5%; Score 672; DB 7; Length 550;
Best Local Similarity 33.1%; Pred. No. 3.6e-28;
Matches 177; Conservative 80; Mismatches 161; Indels 116; Gaps 16;

QY 10 YYELHETIGGPAKVKLACHILTGEMVAIKMDKNTLGS--DLPRIKTEIEALKNLRHQ 67
Db 17 HYTLGDTLGVGTGKVKVGHKLTGHKVAVKILNRQKIRSLDVVGKIRREIQNLKLFRRHP 76
QY 68 HICQLYHVLGTANKI FMWLEYPGCGELFDYIISQDRLSEETRVVFRQIVSAVAVYHSQG 127
Db 77 HIILYQVISTPDSI FWMVEYVSGGELFDYICNGRLDEKESRRLFQQLISGVYDCHRM 136
QY 128 YAHRLDKPENLLPDEYHKLKLIDFGLCAKPKGNKYHLQTCGSLAYAAPELIQGSYLG 187
Db 137 VVHRDLKPEVLLDAHNAKIADPGLSNMDSGE--FLRTSCGSPNYAAPEVISGRLYAG 194
QY 188 SEADVSMGILLYVLMCGELFPDDDDNMYALKYKIMRGKYDVPKWLSPSSILLQOOLQVD 247
Db 195 PEVDIWSGGVILYALLCGTLFPDDDDHVPFTLFRKICDGIFFYTPQYLNPSVISLKLHMLQVD 254
QY 248 PKKRISMKNLNHPWIMQD---YNYPVWQSKNPFILHDDDCVTEL-----S 291
Db 255 PMKRASIKDIRHEHWFQDLPKYLPFDPSPYSSTMI--DDEALKEVCEKPECSEEEVLSC 312
QY 292 VHRN-----NRQTMEDL-----ISLWQYDHLT-----ATYLLLL 321
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Db 313 LYNRNHQDPLAVAYHLIIDNRIRMEAKOFYLATSPDSDLDDHHLTRPHERVPELVAE 372
QY 322 AKKAR-----GKPVRLRLSSFCGQASATPPTDIDKSN-----NW----- 355
Db 373 TPRARHTLDELNPQKSHQGVRAKAKWHLGIRSRPNDAEVCRAIKQLDYEWKVNPNY 432
QY 356 -----SLEDVTASDKNYYVAGIYDWCEDDLS---TGAATP----- 388
Db 433 YLRVRKRNPNVTSTYKMSLQLYQVDSRTY---LLDFRSIDDEITEAKSGTATPQRSGSVS 499
QY 389 --TTSQFTKYWTESNGVESK-SLTPALCRTPANKLKNKENVYTPKSAVKNEEYF 439
Db 490 NYRSCORSDDAEAGKSESVLTSV-----TSLDSSPVDLTPRPGSHSTIEFF 538

RESULT 4
US-11-145-471-12
; Sequence 12, Application US/11145471
; Publication No. US20060147947A1
; GENERAL INFORMATION:
; APPLICANT: Apfeld, Javier
; APPLICANT: O'Conner, Gregory
; TITLE OF INVENTION: AMPK Pathway Components
; FILE REFERENCE: 13407-0570011
; CURRENT APPLICATION NUMBER: US/11/145,471
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: PCT/US/2003/38628
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/430,804
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/578,804
; PRIOR FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 12
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-145-471-12

Query Match 19.4%; Score 669; DB 7; Length 548;
Best Local Similarity 35.9%; Pred. No. 5.1e-28;
Matches 165; Conservative 73; Mismatches 145; Indels 76; Gaps 12;

QY 10 YYELHETIGTGGAFAKVKLACHILTGEMVAIKMDKNTLGS--DLPRKTEIEALKNLRHQ 67
Db 15 HYILGDTLGVGTGKVKVGKHELTGHKVAVKILNRQKIRSLDVVGKIRREIQNLKLFHRP 74
QY 68 HICQLYHVLETANKIPMWLEPCPGELFDYIISQDRLSSEETRVVPRQIVSAVAYVHSQ 127
Db 75 HIILKLVQVISTPDSIPFMVMEYVSGGELFDYICKNGLDEKESRLFPQQLISGVYDYCHRM 134
QY 128 YAHRLDKPENLLFDEYHKLKLDIFGLCAKPKGNKDYHLOTCCGSLAYAAPELIQKSYLG 187
Db 135 VVHRDLKPNVLLDAHNAKIADFGLSNMMSDGE--FLRTSCGSPNYAAPEVISGRLYAG 192
QY 188 SEADVMSGILLVLMCGFLPFDDNNVMALYKKIMRGKYDVPKWLSPSSILLQOQMLQVD 247
Db 193 PEVDIWSGGVILYALLCGTLFPDDHVPPTLFKKICDGIFFYTPQYLNPSVISLLKHLQVD 252
QY 248 PKKRISMKVLLNHPWIMQD---YNPVQSKNPFHLLDDCCVTEL-----S 291
Db 253 PMKRATIKDIREHWFQKDLPKYLFPEDPSPYSSTMI--DDEALKVCEKFECESEEVLS 310
QY 292 VVHRN-----NRQTMEDL-----ISLWQYDHLT-----ATYLLLL 321
Db 311 LYNRNHQDPLAVAYHLIIDNRIRMEAKOFYLATSPDSDLDDHHLTRPHERVPELVAE 370
QY 322 AKKAR-----GKPVRLRLSSFCGQASATPPTDIDKSNWNSLEDVTASDKNYVAGL 371

RESULT 6
US-10-449-902-45099

Db 371 TPRARHTLDELNPQKSHQGVRAKAKWHLGIRSRPNDAEVCRAIKQ----- 419
QY 372 IDYDWCEDD---LSTGAATPRTSQFTKYWTESNGVESKS 407
Db 420 LDYEWKVNPNPYLVRVRKRNPNVTSTFSKMSLQLYQVDSRT 458

RESULT 5
US-11-145-471-18
; Sequence 18, Application US/11145471
; Publication No. US20060147947A1
; GENERAL INFORMATION:
; APPLICANT: Apfeld, Javier
; APPLICANT: O'Conner, Gregory
; TITLE OF INVENTION: AMPK Pathway Components
; FILE REFERENCE: 13407-0570011
; CURRENT APPLICATION NUMBER: US/11/145,471
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: PCT/US/2003/38628
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/430,804
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/578,804
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 60/578,804
; PRIOR FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 18
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-145-471-18

Query Match 19.4%; Score 669; DB 7; Length 548;
Best Local Similarity 35.9%; Pred. No. 5.1e-28;
Matches 165; Conservative 73; Mismatches 145; Indels 76; Gaps 12;

QY 10 YYELHETIGTGGAFAKVKLACHILTGEMVAIKMDKNTLGS--DLPRKTEIEALKNLRHQ 67
Db 15 HYILGDTLGVGTGKVKVGKHELTGHKVAVKILNRQKIRSLDVVGKIRREIQNLKLFHRP 74
QY 68 HICQLYHVLETANKIPMWLEPCPGELFDYIISQDRLSSEETRVVPRQIVSAVAYVHSQ 127
Db 75 HIILKLVQVISTPDSIPFMVMEYVSGGELFDYICKNGLDEKESRLFPQQLISGVYDYCHRM 134
QY 128 YAHRLDKPENLLFDEYHKLKLDIFGLCAKPKGNKDYHLOTCCGSLAYAAPELIQKSYLG 187
Db 135 VVHRDLKPNVLLDAHNAKIADFGLSNMMSDGE--FLRTSCGSPNYAAPEVISGRLYAG 192
QY 188 SEADVMSGILLVLMCGFLPFDDNNVMALYKKIMRGKYDVPKWLSPSSILLQOQMLQVD 247
Db 193 PEVDIWSGGVILYALLCGTLFPDDHVPPTLFKKICDGIFFYTPQYLNPSVISLLKHLQVD 252
QY 248 PKKRISMKVLLNHPWIMQD---YNPVQSKNPFHLLDDCCVTEL-----S 291
Db 253 PMKRATIKDIREHWFQKDLPKYLFPEDPSPYSSTMI--DDEALKVCEKFECESEEVLS 310
QY 292 VVHRN-----NRQTMEDL-----ISLWQYDHLT-----ATYLLLL 321
Db 311 LYNRNHQDPLAVAYHLIIDNRIRMEAKOFYLATSPDSDLDDHHLTRPHERVPELVAE 370
QY 322 AKKAR-----GKPVRLRLSSFCGQASATPPTDIDKSNWNSLEDVTASDKNYVAGL 371

RESULT 6
US-10-449-902-45099


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Db 135 VVRDLKPENLVLDHAKNAKADFGLSNMMSDGE--FLRTSCGSPNYAAPEVISGRLYAG 192
Qy 188 SEADVMSGILLVLMCGFLPFDDNNMVALYKIMRGKYDVPKWLSPSSILLIQOMLQVD 247
Db 193 PEVDIWSGVLVYALLCGTLFPDDEHVPTLFKKIRGGVFYIPEYLNRSVATLLMHMLQVD 252
Qy 248 PKKRISMKNLNHPWIMQD---YNYPVWQSKNPFTH---LDDCVTELSVHHR--NNROT 300
Db 253 PLKGRATIKDIRHEWFKQDLPSTLFP-----EDPSYDANVIDDEAVKEVCEKPECTESEV 307
Qy 301 MEDLISLWQYDHLTATYLLLL 321
Db 308 MNSLYSGDPQDQLAVAYHLII 328

RESULT 9
US-11-145-471-36
; Sequence 36, Application US/11145471
; Publication No. US20060147947A1
; GENERAL INFORMATION:
; APPLICANT: Apfeld, Javier
; TITLE OF INVENTION: AMPK Pathway Components
; FILE REFERENCE: 13407-0570011
; CURRENT APPLICATION NUMBER: US/11/145,471
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: PCT/US/2003/38628
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/430,804
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: US 60/488,261
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 60/578,804
; PRIOR FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 36
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-145-471-36

Query Match 18.7%; Score 644; DB 7; Length 552;
Best Local Similarity 43.3%; Pred. No. 1.1e-26;
Matches 139; Conservative 50; Mismatches 116; Indels 16; Gaps 6;

Qy 10 YYELHETIGTGGAFAKVKLACHILTGEMVAIKIMDKNTLGS--DLPRIKTEIEALKNLRHQ 67
Db 15 HYVLGDTLGVGTGKVKIGEHQLTGHKVAVKILNRKIRSLDVGKIKREIQNLKLFHRP 74
Qy 68 HICQLYHVLGTANKIFWVLEYPGGLFDYIISQDRLSSEETRVVFRQIVSAVAVYHSG 127
Db 75 HIKLVQVISTPTDFWVWEYVSGGLFDYICXGRVEVEARLFFQQLSADVYCHRM 134
Qy 128 YAHRLKPNLFLDEYHKLKLIDFGICAKPKGNKDYHLQTCGSLAYAAPELIQGSYLG 187
Db 135 VVRDLKPENLVLDHAKNAKADFGLSNMMSDGE--FLRTSCGSPNYAAPEVISGRLYAG 192
Qy 188 SEADVMSGILLVLMCGFLPFDDNNMVALYKIMRGKYDVPKWLSPSSILLIQOMLQVD 247
Db 193 PEVDIWSGVLVYALLCGTLFPDDEHVPTLFKKIRGGVFYIPEYLNRSVATLLMHMLQVD 252
Qy 248 PKKRISMKNLNHPWIMQD---YNYPVWQSKNPFTH---LDDCVTELSVHHR--NNROT 300
Db 253 PLKGRATIKDIRHEWFKQDLPSTLFP-----EDPSYDANVIDDEAVKEVCEKPECTESEV 307
Qy 301 MEDLISLWQYDHLTATYLLLL 321
Db 308 MNSLYSGDPQDQLAVAYHLII 328

RESULT 10
US-11-145-471-37
; Sequence 37, Application US/11145471
; Publication No. US20060147947A1
; GENERAL INFORMATION:
; APPLICANT: Apfeld, Javier
; TITLE OF INVENTION: AMPK Pathway Components
; FILE REFERENCE: 13407-0570011
; CURRENT APPLICATION NUMBER: US/11/145,471
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: PCT/US/2003/38628
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/430,804
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: US 60/488,261
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 60/578,804
; PRIOR FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 37
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-145-471-37

Query Match 18.7%; Score 644; DB 7; Length 552;
Best Local Similarity 43.3%; Pred. No. 1.1e-26;
Matches 139; Conservative 50; Mismatches 116; Indels 16; Gaps 6;

Qy 10 YYELHETIGTGGAFAKVKLACHILTGEMVAIKIMDKNTLGS--DLPRIKTEIEALKNLRHQ 67
Db 15 HYVLGDTLGVGTGKVKIGEHQLTGHKVAVKILNRKIRSLDVGKIKREIQNLKLFHRP 74
Qy 68 HICQLYHVLGTANKIFWVLEYPGGLFDYIISQDRLSSEETRVVFRQIVSAVAVYHSG 127
Db 75 HIKLVQVISTPTDFWVWEYVSGGLFDYICXGRVEVEARLFFQQLSADVYCHRM 134
Qy 128 YAHRLKPNLFLDEYHKLKLIDFGICAKPKGNKDYHLQTCGSLAYAAPELIQGSYLG 187
Db 135 VVRDLKPENLVLDHAKNAKADFGLSNMMSDGE--FLRTSCGSPNYAAPEVISGRLYAG 192
Qy 188 SEADVMSGILLVLMCGFLPFDDNNMVALYKIMRGKYDVPKWLSPSSILLIQOMLQVD 247
Db 193 PEVDIWSGVLVYALLCGTLFPDDEHVPTLFKKIRGGVFYIPEYLNRSVATLLMHMLQVD 252
Qy 248 PKKRISMKNLNHPWIMQD---YNYPVWQSKNPFTH---LDDCVTELSVHHR--NNROT 300
Db 253 PLKGRATIKDIRHEWFKQDLPSTLFP-----EDPSYDANVIDDEAVKEVCEKPECTESEV 307
Qy 301 MEDLISLWQYDHLTATYLLLL 321
Db 308 MNSLYSGDPQDQLAVAYHLII 328

RESULT 11
US-10-449-902-50922
; Sequence 50922, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50922
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-50922

Query Match      18.6%; Score 640.5; DB 6; Length 509;
Best Local Similarity 36.9%; Pred. No. 1.5e-26;
Matches 149; Conservative 64; Mismatches 118; Indels 73; Gaps 10;

QY      4 YDELLKYYELHETIGTGGFAKVKLACHILTGENVAIKMDKNTLGS--DLPRIKTEIAL 61
Db      10 HSEALKNYNLGRTLGIGSGFKVIAEHKLTGHRVAIKILNRQRMRNMEMEAKREIKIL 69

QY      62 KNLRHQHI COLYHVLE TANKI FMWLEYCPGGELFDYIISQDRLSEETRVVFRQIVSAVA 121
Db      70 RLFPHIIRLYEVIYTPTDIYVMVEYCKFGELFDYIVEKGRLODEARRIFQOIISGYE 129

QY      122 YVHSQGYAHRDLKPENLLFDEYHKLIDFGLCAKPKGNKYDVPKWLSPSSILLIQ 181
Db      130 YCHRNMMVVRDLKPENLLDLSKYNVKLADPGL--SNVMHDGHFLKTS CGSPNYAAPEVIS 187

QY      182 GKSYLEGSEADVMSGMILLYVLMCGFLPFDDNNMVALYKKIMRGKYDVPKWLSPSSILLIQ 241
Db      188 GKLYAGPEVDVMSGVIYVALLCGTLPFDDDENIPNLFKIKGGIYTLPSHLSALARDLIP 247

QY      242 QMLQVDPKGRISMKNLNHPIMQDYNYP-----VEWQSKNPFHILDDCVTELSV 292
Db      248 RMLVVDPMKRITIREHQWF--QIRLPYLA VPPPTAQQAQ-----MIDED----- 294

QY      293 HHRNNQTMEDLISL-WQYDHL-----TATYLLLLAKKARG-----KP 329
Db      295 -----TLQDVVNLGYEKDHVCESLRNRLQNEATVAYLLLDNFRFRATSGYLADYQES 347

QY      330 VRLRLSSFCGQASATPFTDIKSNMWSLEDVTASDKNYVAGLID 373
Db      348 LERNLRFA-----SSASASNTRHYPGSSD 374

RESULT 13
US-10-449-902-47226
; Sequence 47226, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47226
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-47226

Query Match      18.5%; Score 637.5; DB 6; Length 548;
Best Local Similarity 37.9%; Pred. No. 2.3e-26;
Matches 151; Conservative 62; Mismatches 124; Indels 61; Gaps 11;

QY      4 YDELLKYYELHETIGTGGFAKVKLACHILTGENVAIKMDKNTLGS--DLPRIKTEIAL 61
Db      53 HSEALKNYNLGRTLGIGSGFKVIAEHKLTGHRVAIKILNRQRMRNMEMEAKREIKIL 112

QY      62 KNLRHQHI COLYHVLE TANKI FMWLEYCPGGELFDYIISQDRLSEETRVVFRQIVSAVA 121
Db      113 RLFPHIIRLYEVIYTPTDIYVMVEYCKFGELFDYIVEKGRLODEARRIFQOIISGYE 172

QY      122 YVHSQGYAHRDLKPENLLFDEYHKLIDFGLCAKPKGNKYDVPKWLSPSSILLIQ 181
Db      173 YCHRNMMVVRDLKPENLLDLSKYNVKLADPGL--SNVMHDGHFLKTS CGSPNYAAPEVIS 230

QY      182 GKSYLEGSEADVMSGMILLYVLMCGFLPFDDNNMVALYKKIMRGKYDVPKWLSPSSILLIQ 241
Db      231 GKLYAGPEVDVMSGVIYVALLCGTLPFDDDENIPNLFKIKGGIYTLPSHLSALARDLIP 290

QY      242 QMLQVDPKGRISMKNLNHPIMQDYNYP-----VEWQSKNPFHILDDCVTELSV 292
Db      291 RMLVVDPMKRITIREHQWF--QIRLPYLA VPPPTAQQAQ-----MIDED----- 337
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